

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:39:11 ; Search time 231 Seconds

(without alignment)  
494.786 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDAIPAVEFEGEP.....VEPDGTGLTSLAPNISQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot\_05.80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	214	1	PRDX5_HUMAN
2	830	100.0	214	2	PRDX5_HUMAN
3	822	99.0	215	1	PRDX5_GERAE
4	818	98.6	215	1	PRDX5_PAPHA
5	767	92.4	210	1	PRDX5_MOUSE
6	767	92.4	213	1	PRDX5_RAT
7	763	91.9	213	2	PRDX5_RAT
8	761	91.7	162	2	PRDX5_PIG
9	747	90.0	219	1	PRDX5_BOVIN
10	727	87.6	211	2	PRDX5_MOUSE
11	583.5	70.3	189	2	PRDX5_XENLA
12	536.5	64.6	162	2	PRDX5_BRARE
13	524	63.1	188	2	PRDX5_BRARE
14	494.5	59.6	157	2	PRDX5_BRARE
15	486.5	58.6	246	2	PRDX5_MOUSE
16	484	58.3	168	2	PRDX5_MOUSE
17	483	58.2	157	2	PRDX5_MOUSE
18	481	58.0	190	2	PRDX5_MOUSE
19	475.5	57.3	175	2	PRDX5_MOUSE
20	408	49.2	89	2	PRDX5_MOUSE
21	400.5	48.3	185	2	PRDX5_MOUSE
22	355.5	42.8	184	2	PRDX5_MOUSE
23	354.5	42.7	220	2	PRDX5_MOUSE
24	354.5	42.7	220	2	PRDX5_MOUSE
25	341.5	41.1	167	2	PRDX5_MOUSE
26	341.5	41.1	183	2	PRDX5_MOUSE
27	337.5	40.7	167	2	PRDX5_MOUSE
28	336.5	40.5	188	2	PRDX5_MOUSE
29	321	38.7	168	2	PRDX5_MOUSE
30	318.5	38.4	185	2	PRDX5_MOUSE
31	317	38.2	161	2	PRDX5_MOUSE

32	317	38.2	191	2	PRDX5_MOUSE
33	314	37.8	161	2	PRDX5_MOUSE
34	312.5	37.4	160	2	PRDX5_MOUSE
35	310.5	37.4	160	2	PRDX5_MOUSE
36	310	37.3	314	2	PRDX5_MOUSE
37	309	37.2	197	2	PRDX5_MOUSE
38	308.5	37.2	196	2	PRDX5_MOUSE
39	308	37.1	157	2	PRDX5_MOUSE
40	307.5	37.0	161	2	PRDX5_MOUSE
41	307.5	37.0	168	2	PRDX5_MOUSE
42	305	36.7	158	2	PRDX5_MOUSE
43	304.5	36.7	168	2	PRDX5_MOUSE
44	304	36.6	159	2	PRDX5_MOUSE
45	303	36.5	161	2	PRDX5_MOUSE

#### ALIGNMENTS

PRDX5_HUMAN	STANDARD	PRT	214 AA.
AC	P30044; Q9UBU5; Q9UBU4; Q9UKX4;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Peroxiredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Pxx-V)		
DE	(Peroxisomal antioxidant enzyme) (PAP) (Thioredoxin reductase)		
DE	(Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOB166)		
DE	(TPX type VI) (Liver tissue 2D-page spot 71B) (Alu corepressor 1).		
GN	Name=PRDX5; Synonyms=ACR1; ORFNames=SB110;		
OS	Homo sapiens (Human).		
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Kim I.H., Jeong W.,		
RT	"A new type of human thiol peroxidase (Human TPX type VI)."		
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=20145535; PubMed=10679306; DOI=10.1006/brc.2000.2231;		
RA	Zhou Y., Kok K.H., Chun A.C.S., Wong C.M., Wu H.W., Lin M.C.M.,		
RT	"Mouse peroxidoredoxin V is a thioredoxin peroxidase that inhibits p53-		
RL	induced apoptosis."		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.		
RX	MEDLINE=99445545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;		
RA	Yamashita H., Ayerham S., Jiang S., London R., Van Veldhoven P.P.,		
RT	"Characterization of human and murine PMP20 peroxisomal proteins that		
RL	exhibit antioxidant activity in vitro."		
RN	[4]		
RP	NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.		
RC	TISSUE=lung;		
RX	MEDLINE=9945929; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;		
RA	Knoops B., Clipse A., Bogard C., Aralane K., Wattiez R., Hermans C.,		
RT	"Cloning and characterization of AOB166, a novel mammalian		
RL	antioxidant enzyme of the peroxidoredoxin family."		
RN	[5]		
RP	NUCLEOTIDE SEQUENCE, MUTAGENESIS, AND CHARACTERIZATION.		
RX	MEDLINE=20347113; PubMed=10751410; DOI=10.1074/jbc.M001943200;		
RA	Seo M.S., Kang S.W., Kim K., Baines I.C., Lee T.H., Rhee S.G.,		
RT	"Identification of a new type of mammalian peroxidoredoxin that forms an		
RL	intramolecular disulfide as a reaction intermediate."		
RN	J. Biol. Chem. 275:20346-20354(2000).		

RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99195471; PubMed=10095767;  
 RA Kropotov A., Sedova V., Ivanov V., Sazeeva N., Tomilin A.,  
 RA Krutikina R., Oel S.L., Griesenbeck J., Buchlow G., Tomilin N.;  
 RT "A novel human DNA-binding protein with sequence similarity to a  
 RT subfamily of redox proteins which is able to repress RNA-polymerase-  
 RT III-driven transcription of the Alu-family retroposons in vitro.";   
 RL Eur. J. Biochem. 260:336-346(1999).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RX TISSUE=Adrenal gland;  
 RC MEDLINE=20402571; PubMed=10931946; DOI=10.1073/pnas.160270997;  
 RA Hu Z.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,  
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Pu G., Zhang Q.-H.,  
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Kong R., Ye M., Zhou J.,  
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,  
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;  
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal  
 RT axis and full-length cDNA cloning.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RA Zhang W., Li N., Wan T., Cao X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP PROTEIN SEQUENCE OF 54-63.  
 RC TISSUE=Liver;  
 RX MEDLINE=93162045; PubMed=1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargass R.,  
 RA Appel R.D., Hughes G.J.;  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";   
 RL Electrophoresis 13:992-1001(1992).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RX MEDLINE=21410064; PubMed=11518528; DOI=10.1006/jmbi.2001.4853;  
 RA Declercq J.-P., Byrard C., Clippe A., Stricht D.V., Bernard A.,  
 RA Knoops B.;  
 RT "Crystal structure of human peroxiredoxin 5, a novel type of mammalian  
 RT peroxiredoxin at 1.5-A resolution.";   
 RL J. Mol. Biol. 311:751-759(2001).  
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with  
 CC reducing equivalents provided through the thioredoxin system.  
 CC Involved in intracellular redox signaling.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, Mitochondrial (shown here) and  
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL, AJ249483, CAB62210.1, -, mRNA.  
 CC EMBL, AF197952, AAF04856.1, -, mRNA.  
 CC EMBL, AF124993, AAF27531.1, -, mRNA.  
 CC EMBL, AF110731, AAF03750.1, -, mRNA.  
 CC EMBL, AF231705, AAF78899.1, -, mRNA.  
 CC EMBL, AF112212, AAF17200.1, -, mRNA.  
 CC EMBL, AF242525, AAF9605.1, -, mRNA.  
 CC PDB, 1H40, X-ray, A/B/C/D/E/F/G/H=54-214.  
 CC PDB, 1HD2, X-ray, A=54-214.  
 CC PDB, 1OC3, X-ray, A/B/C=54-214.  
 CC PDB, 1URM, X-ray, A=54-214.

DR SWISS-2DPAGE; P30044; HUMAN.  
 DR OGP: P30044; -;  
 DR EMBL; ENSG00000126432; Homo sapiens.  
 DR HGN; HGN:9355; PRDX5.  
 DR H-INVD; HIX0021287; -;  
 DR MIM; 606583; -;  
 DR GO; GO:0005739; C:mitochondrion; TAS.  
 DR GO; GO:0005777; C:peroxisome; TAS.  
 DR GO; GO:0005489; F:electron transporter activity; TAS.  
 DR GO; GO:0006954; P:inflammatory gaseous exchange; TAS.  
 DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.  
 DR GO; GO:0006979; P:response to oxidative stress; TAS.  
 DR InterPro; IPR000866; AtpC-TSA.  
 DR InterPro; IPR012335; Thioredoxin-like.  
 DR InterPro; IPR0578; AtpC-TSA; 1.  
 DR Pfam; PF00578; AtpC-TSA; 1.  
 KW 3D-structure; Alternative initiation; Antioxidant;  
 KW Direct protein sequencing; Mitochondrion; Oxidoreductase; Peroxidase;  
 KW Peroxisome; Polymorphism; Redox active center; Transil peptide.  
 FT TRANSIT 1 ?  
 FT INT MET 53 53  
 FT CHAIN 54 214  
 FT CHAIN ? 214  
 FT MOTIF 212 214  
 FT DISULFID 100 204  
 FT VARIANT 141 141  
 FT MUTAGEN 100 100  
 FT MUTAGEN 125 125  
 FT MUTAGEN 204 204  
 FT TURM 58 59  
 FT STRAND 61 61  
 FT STRAND 66 68  
 FT TURM 72 73  
 FT STRAND 75 77  
 FT HELIX 78 81  
 FT TURM 82 84  
 FT STRAND 86 92  
 FT TURM 95 96  
 FT HELIX 98 102  
 FT TURM 103 103  
 FT HELIX 104 110  
 FT TURM 111 111  
 FT HELIX 112 116  
 FT TURM 117 119  
 FT STRAND 122 127  
 FT HELIX 131 140  
 FT TURM 141 142  
 FT STRAND 144 146  
 FT STRAND 148 151  
 FT TURM 153 154  
 FT HELIX 156 161  
 FT TURM 162 162  
 FT STRAND 164 164  
 FT HELIX 168 173  
 FT STRAND 178 178  
 FT STRAND 181 186  
 FT TURM 187 188  
 FT STRAND 189 195  
 FT TURM 197 198  
 FT TURM 204 205  
 FT HELIX 214 214  
 SQ SEQUENCE 214 AA; 22026 MW; 2FF211210809823E CRC64;  
 Query Match 100.0%; Score 830; DB 1; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 9,56-66;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPIRVGDAIPAVEVEFEGEPGNKVNIAELFKGKKGVLFQVPGAFTPGCSKTHLPQVEQA 60  
 |||

Db 53 MAPIKVGAIPAVEFESEPGNKVNLAELFKGKGVLFVPGAFPTGCKTHLPGFVQA 112  
 QY 61 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 120  
 Db 113 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 172  
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 162  
 Db 173 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 214

## RESULT 2

OGIAF2 HUMAN  
 ID OGIAF2 HUMAN PRELIMINARY; PRT; 214 AA.

AC OGIAF2  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DE PRDX5 protein.  
 GN Name=PRDX5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 DR EMBL; CRA57203; CAC33484.1; -, mRNA.  
 DR SMR; OGIAF2; 54-214.  
 DR Ensembl; ENSG00000126432; Homo sapiens.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioresoxin-like.  
 DR InterPro; IPR012335; Thioresoxin-fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
 SQ SEQUENCE 214 AA; 22026 MW; 2PR21121080923E CRC64;

Query Match 100.0%; Score 830; DB 2; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-66;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGAIPAVEFESEPGNKVNLAELFKGKGVLFVPGAFPTGCKTHLPGFVQA 60  
 Db 53 MAPIKVGAIPAVEFESEPGNKVNLAELFKGKGVLFVPGAFPTGCKTHLPGFVQA 112  
 QY 61 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 120  
 Db 113 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 172  
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 162  
 Db 173 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 214

## RESULT 3

PRDX5 CERAE  
 ID PRDX5 CERAE STANDARD; PRT; 215 AA.

AC OGGLW7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)  
 DE (Thioredoxin reductase).  
 GN Name=PRDX5;  
 OS Cercopithecus aethiops (Green monkey) (Griwet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheciidae; Cercopithecinae; Cercopithecus.  
 NCBI\_TaxID=9534;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RA Knops B., Cherif H.;  
 RT Cloning and characterization of COS-7 AOB166/PRDX5.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Reduces hydrogen peroxide and alky1 hydroperoxides with  
 reducing equivalents provided through the thioredoxin system.  
 CC Involved in intracellular redox signaling (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic  
 CC (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, Mitochondrial (shown here) and  
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.

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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC EMBL; AF110736; AAG13453.2; -, mRNA.  
 CC HSSP; P30044; 1HD2.  
 DR SMR; OGGLW7; 55-215.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioresoxin-like.  
 DR InterPro; IPR012335; Thioresoxin-fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;  
 KW Peroxidase; Peroxisome; Redox-active center; Transist peptide.  
 FT TRANSIT 1 ? Mitochondrion (potential).  
 FT INTR\_MET 54 54 For isoform Cytoplasmic+peroxisomal.  
 FT CHAIN 55 215 Peroxiredoxin 5, isoform  
 FT CHAIN ? 215 Cytoplasmic+peroxisomal.  
 FT MOTIF 213 215 Peroxiredoxin 5, isoform Mitochondrial.  
 FT MOTIF 213 215 Microbody targeting signal (By  
 FT DISULFID 101 205 similarity). (By similarity).  
 FT REDOX 213 215 Redox-active.  
 SQ SEQUENCE 215 AA; 22237 MW; 7C9B45C1B9517B78 CRC64;

Query Match 99.0%; Score 822; DB 1; Length 215;  
 Best Local Similarity 98.8%; Pred. No. 4.9e-65;  
 Matches 160; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGAIPAVEFESEPGNKVNLAELFKGKGVLFVPGAFPTGCKTHLPGFVQA 60  
 Db 54 MAPIKVGAIPAVEFESEPGNKVNLAELFKGKGVLFVPGAFPTGCKTHLPGFVQA 113  
 QY 61 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 120  
 Db 114 EALRAKGVQVVAACSVNDAFVTGEMGRAHKAEGKVRLLADPTGAGKGTDLILDLSVSI 173  
 QY 121 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 162  
 Db 174 FGNRLKRFMSWVODGIVKALNVEPDGTGTCSLAPNIISQI 215

## RESULT 4

PRDX5 PAPHA  
 ID PRDX5 PAPHA STANDARD; PRT; 215 AA.

AC OGGLW5;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peroxiredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)  
 DE (Thioredoxin reductase).  
 GN Name=PRDX5;  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheciidae; Cercopithecinae; Papio.

OX NCBI\_TaxID=9557;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Knoops B., Cherif H.;  
 RT "Cloning and characterization of baboon AOEB166/PRDX5."  
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with  
 CC reducing equivalents provided through the thioredoxin system.  
 CC Involved in intracellular redox signaling (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic  
 CC (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative initiation;  
 CC Comment-2 isoforms, Mitochondrial (shown here) and  
 CC Cytoplasmic-peroxisomal, are produced by alternative initiation;  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: AF110734; AAC13451.2; -, mRNA.  
 CC HSSP: P30044; 1HD2.  
 DR SMR: O9GLM9; S5-215.  
 DR InterPro: IPR000866; Ahpc-TSA.  
 DR InterPro: IPR012336; Thioredoxin-like.  
 DR Pfam: PF00578; Ahpc-TSA; 1.  
 DR Pfam: PF00578; Ahpc-TSA; 1.  
 KM Alternative initiation; Antioxidant; Mitochondrial; Oxidoreductase;  
 KM Peroxidase; Peroxisome; Redox-active center; Transil peptide.  
 FT TRANSIT 1 ? Mitochondrion (potential).  
 FT INIT MET 54 54 For isoform Cytoplasmic+peroxisomal.  
 FT CHAIN 55 215 Peroxiredoxin 5, isoform  
 FT MOTIF 213 215 Cytoplasmic+peroxisomal.  
 FT MOTIF 213 215 Peroxiredoxin 5, isoform Mitochondrial.  
 FT MOTIF 213 215 Microbody targeting signal (By  
 FT MOTIF 213 215 similarity).  
 FT DISULFID 101 205 Redox-active (By similarity).  
 FT SEQUENCE 215 AA; 22166 MW; 65183A24535C1617 CRC64;  
 SQ  
 Best Match 98.6%; Score 818; DB 1; Length 215;  
 Query Local Similarity 98.1%; Pred. No. 1,1e-64;  
 Matches 159; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAPIKVDAIPAVEVEGEPGNKVNLAELFKGKGVLPVPGAFTPGCSKTHLPGFVEQA 60  
 DB 54 MAPIKVDAIPAVEVEGEPGNKVNLAELFKGKGVLPVPGAFTPGCSKTHLPGFVEQA 113  
 QY 61 EALKAGVGVVACTLVNDAAFVTGEMGRARAKREKRVLLADPTGAFKEKTDLLDLSLVI 120  
 DB 114 EALKAGVGVVACTLVNDAAFVTGEMGRARAKREKRVLLADPTGAFKEKTDLLDLSLVI 173  
 QY 121 FGNRRLRKFSMVVQDGIIVKALNVEPDGTGLTSLAPNISQL 162  
 DB 174 FGNRRLRKFSMVVQDGIIVKALNVEPDGTGLTSLAPNISQL 215  
 RESULT 5  
 PRDX5 MOUSE STANDARD; PRT; 210 AA.  
 ID PRDX5\_MOUSE  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peroxisomal oxidant 5, mitochondrial precursor (BC 1.11.1.15) (Prx-V)  
 DE (Thioredoxin peroxidase PMP20) (Antioxidant enzyme B166) (AOEB166)  
 DE (Liver tissue 2D-page spot 2D-00141V).  
 GN Name=Prdx5; Synonyms=Prdx6;

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.  
 RP MEDLINE=20145535; PubMed=10679306; DOI=10.1006/birc.2000.2231;  
 RA Zhou Y., Kok K.H., Chun A.C.S., Wong C.M., Wu H.W., Lin M.C.M.,  
 RA Fung P.C.W., Kung H.-F., Jin D.-Y., Jin D.-Y.;  
 RT "Mouse peroxiredoxin V is a thioredoxin peroxidase that inhibits p53-  
 RT induced apoptosis."  
 RT Biochem. Biophys. Res. Commun. 268:921-927(2000).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.  
 RP MEDLINE=99445545; PubMed=10514471; DOI=10.1074/jbc.274.42.29897;  
 RA Yamashita H., Avraham S., Jiang S., London R., Van Veldhoven P.P.,  
 RA Subramani S., Rogers R.A., Avraham H.;  
 RT "Characterization of human and murine PMP20 peroxisomal proteins that  
 RT exhibit antioxidant activity in vitro."  
 RL J. Biol. Chem. 274:29897-29904(1999).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=C3H/HeJ; TISSUE=Lung;  
 RA MEDLINE=99445545; PubMed=10514471; DOI=10.1074/jbc.274.43.30451;  
 RA Knoops B., Clippe A., Bogard C., Arsalane K., Wattiez R., Hermans C.,  
 RA Ducousselle E., Falmagne P., Bernard A.;  
 RT "Cloning and characterization of AOEB166, a novel mammalian  
 RT antioxidant enzyme of the peroxiredoxin family."  
 RL J. Biol. Chem. 274:30451-30458(1999).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20218665; PubMed=10753630; DOI=10.1006/birc.2000.2430;  
 RA Lee T.H., Kim S.J., Kang S.W., Lee K.K., Rhee S.G., Yu D.Y.;  
 RT "Molecular cloning and characterization of the mouse Peroxiredoxin V  
 RT gene."  
 RL Biochem. Biophys. Res. Commun. 270:356-362(2000).  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=22354683; PubMed=12466651; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Oshio N., Saito R., Suzuki H., Yamashita H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Knapin A., Matsumura H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazee K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numa K., Okido T., Pavan W.D., Pereira G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J.P., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imocani K., Iehli Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Mammary tumor;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, H.  
1, R.R.; Melakanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82051  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-247 <HE>  
A:Cross-references: UNIPROT:Q9KNU3; UNIPARC:UPI00000C3360; GB:AE004330; GB:AE003852; NIT  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC2637  
A:Map position: 1

Query Match 29.3%; Score 243.5; DB 2; Length 247;  
Best Local Similarity 38.8%; Pred. No. 4.5e-15;  
Matches 57; Conservative 24; Mismatches 61; Indels 5; Gaps 4;  
QY 5 KVGDAIPAV--EVEFEGEPGNKVNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEAL 62  
DB 9 KEGGTIPQVTPPTPGQDAMVAVTSDLELFGKTVIVFSLPGAFPTCCSSHLPRYNELAPVF 68  
QY 63 LKAGVQVAVCLSVNDAFVTGEMGRARABGKVRLLADPTGAFGKETDLLDDSLVSIFG 122  
DB 69 FKEHGVDSILCVSVNDTFVNAMAKDDQAD--NITFIPDNGEFTDGMGLVYKNDLIG-FG 126  
QY 123 NRLLKRFSGNVQDGIYKALNVEPDGTG 149  
DB 127 -KRSWRYSMVLVNGVVEKMFIEPNBPG 152

RESULT 14  
AB0477  
probable peroxiredoxin/glutaredoxin family protein YP03916 [imported] - *Yersinia pestis*  
C:Species: *Yersinia pestis*  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AB0477  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AB0477  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-243 <KUR>  
A:Cross-references: UNIPROT:Q8ZA95; UNIPARC:UPI00000DCAA0; GB:AL590842; PIDN:CAC93382.1;  
C:Genetics:  
A:Gene: YP03916

Query Match 27.2%; Score 225.5; DB 2; Length 243;  
Best Local Similarity 36.6%; Pred. No. 2e-13;  
Matches 53; Conservative 27; Mismatches 60; Indels 5; Gaps 4;

QY 7 GDALPAV--EVEFEGEPGNKVNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEALX 64  
DB 7 GKXVPQVTFHTRQGDQWIDVTTDDLFNSKTVIVFSLPGAFPTCCSSHLPRYNELAGVFX 66  
QY 65 AKGVQVAVCLSVNDAFVTGEMGRARABGKVRLLADPTGAFGKETDLLDDSLVSIFGNR 124  
DB 67 QHGVDSILCVSVNDTFVNAMAKSDQAH--NITFVPDNGEFTKGMMLVERKADLG-FGPR 124  
QY 125 RLKRFSGNVQDGIYKALNVEPDGTG 149  
DB 125 SW-RYSMLVNGVVEKMFIEPNBPG 148

RESULT 15  
I64154  
conserved hypothetical protein HI0572 - *Haemophilus influenzae* (strain Rd KW20)  
C:Species: *Haemophilus influenzae*

C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: I64154  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirschner, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fullmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: I64154  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-241 <TTGR>  
A:Cross-references: UNIPROT:P44758; UNIPARC:UPI0000139ABD; GB:U32739; GB:I42023; NID:915

Query Match 26.4%; Score 219.5; DB 2; Length 241;  
Best Local Similarity 36.3%; Pred. No. 7.3e-13;  
Matches 53; Conservative 27; Mismatches 59; Indels 7; Gaps 5;  
QY 7 GDALPAVEVEFEGEPGNK---VNLAELFKGKGVLFVGPAFTPGCSKTHLPGFVEQAEAL 63  
DB 6 GKXVPQV--TRTRQGDQWIDVTTSDLELFGKTVIVFSLPGAFPTCCSSHLPRYNELAPVF 64  
QY 64 KAKGVQVAVCLSVNDAFVTGEMGRARABGKVRLLADPTGAFGKETDLLDDSLVSIFGN 123  
DB 65 KKGVDVILVSVNDTFVNAMAKDEKSE--NISFIPDNGEFTDGMGLVYKNDLIG-FG- 121  
QY 124 RLKRFSGNVQDGIYKALNVEPDGTG 149  
DB 122 KRSWRYSMVLVNGVVEKMFIEPNBPG 147

Search completed: February 21, 2006, 21:46:54  
Job time : 40 secs



DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioredoxin-like.  
 DR InterPro; IPR012335; Thioredoxin\_fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;  
 KW Peroxidase; Peroxisome; Polymorphism; Redox-active center;  
 KW Transist peptide.  
 FT TRANSIT 1 ? Mitochondrion (potential).  
 FT INIT MET 52 52 For isoform Cytoplasmic+peroxisomal.  
 FT CHAIN 53 213 Peroxisome 5, isoform  
 FT MOTIF 211 213 Cytoplasmic+peroxisomal.  
 FT CHAIN 213 213 Peroxisome 5, isoform Mitochondrial.  
 FT DISUPID 99 203 Redox-active (By similarity).  
 FT VARIANT 68 68 E -> G.  
 FT VARIANT 114 114 L -> P.  
 FT VARIANT 130 130 A -> V.  
 SQ SEQUENCE 213 AA; 22179 MW; 9F0D03A4C87708A CRC64;  
 Query Match 92.4%; Score 767; DB 1; Length 213;  
 Best Local Similarity 90.7%; Pred. No. 3,8e-60;  
 Matches 147; Conservative 7; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MAPKVGDALPAVEVEEGEPGNKVNLAELFKGKGVLPVPGAFTPGCKTHLPGFVEQA 60  
 DB 52 MAPKVGDITPSEVEEGEPGNKVNLAELFKDKKGVLPVPGAFTPGCKTHLPGFVEQA 111  
 QY 61 EALKAGVQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 120  
 DB 112 GALKAKGQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 171  
 QY 121 FGNRLKRFPSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 162  
 DB 172 FGNRLKRFPSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 213  
 RESULT 7  
 Q68G22 RAT PRELIMINARY; PRT; 213 AA.  
 ID Q68G22 RAT PRELIMINARY; PRT; 213 AA.  
 AC Q68G22;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DE Peroxiredoxin 5,.  
 GN Name=Prdx5;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;  
 OC Muridae; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=101116;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schietz T.E.,  
 RA Bivumstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.N., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Spitzer A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilmov J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzyzinski M.I., Skalek U., Smalhus D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA TISSUE=Heart;  
 RA Director MGC Project;  
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 DR EMBL; BC078773; AAH78771.1; -; mRNA.  
 DR SMR; Q68G22; 53-213.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioredoxin-like.  
 DR InterPro; IPR012335; Thioredoxin\_fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
 SQ SEQUENCE 213 AA; 22207 MW; 196A03BC61603825 CRC64;  
 Query Match 91.9%; Score 763; DB 2; Length 213;  
 Best Local Similarity 90.1%; Pred. No. 8.7e-60;  
 Matches 146; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MAPKVGDALPAVEVEEGEPGNKVNLAELFKGKGVLPVPGAFTPGCKTHLPGFVEQA 60  
 DB 52 MAPKVGDITPSEVEEGEPGNKVNLAELFKDKKGVLPVPGAFTPGCKTHLPGFVEQA 111  
 QY 61 EALKAGVQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 120  
 DB 112 GALKAKGQVAVCLSVNDAFTVGEWGRAHKAEGKRYLLADPTGAFGKETDILLDSLVSI 171  
 QY 121 FGNRLKRFPSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 162  
 DB 172 FGNRLKRFPSMVQDGIYKALNVEPDGTGLTCSLAPNIIISQL 213  
 RESULT 8  
 Q6GLW8 PIG PRELIMINARY; PRT; 162 AA.  
 ID Q6GLW8 PIG PRELIMINARY; PRT; 162 AA.  
 AC Q6GLW8;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Peroxiredoxin 5.  
 GN Name=PRDX5;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 OC Sus.  
 NCBI\_Taxid=9823;  
 RX MEDLINE=10521424; DOI=10.1074/jbc.274.43.30451;  
 RA Knops B., Clippe A., Bogard C., Arsalane K., Wattiez R., Hermans C.,  
 RA Ducousset E., Falmagne P., Bernard A.,  
 RT "Cloning and characterization of AOE166, a novel mammalian  
 RT antioxidant enzyme of the peroxiredoxin family";  
 RL J. Biol. Chem. 274:30451-30456 (1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA TISSUE=Liver;  
 RA Knops B., de Wergifosse P., Boone C.,  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 DR EMBL; AF110735; AAG33452.2; -; mRNA.  
 DR HSSP; P30044; 1HD2.  
 DR SMR; Q6GLW8; 2-162.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0004601; F:peroxidase activity; IEA.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioredoxin-like.  
 DR InterPro; IPR012335; Thioredoxin\_fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strauberg R.L., Weinigold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Scheimen C.M., Schuler D.,  
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Scheiner C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,  
 RA Rahn S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bock S.A., McEwen P.J., McKernan K.D., Malek J.A., Gumaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 EN [7]  
 RP PROTEIN SEQUENCE OF 50-61.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,  
 RL Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.,  
 CC Submitted (Aug-1998) to Swiss-Prot.  
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with  
 CC reducing equivalents provided through the thioredoxin system.  
 CC -1- INVOLVED in intracellular redox signaling.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative Initiation;  
 CC Comment=2 isoforms, Mitochondrial (shown here) and  
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL, AF197951; AAF04855.1; -; mRNA.  
 CC EMBL, AF124994; AAF27532.1; -; mRNA.  
 CC EMBL, AF110733; AAG13450.1; -; mRNA.  
 CC EMBL, AF208730; AAF21016.1; -; Genomic DNA.  
 CC EMBL, AF208729; AAF21016.1; JOINED; Genomic DNA.  
 CC EMBL, AK002383; BAB22058.1; -; mRNA.  
 CC EMBL, AK003332; BAB22720.1; -; mRNA.  
 CC EMBL, BC008174; AAB08174.1; -; mRNA.  
 CC PIR, JCT239; JCT239.  
 CC HSSP, P30044; 1HD2.  
 CC SMR, P99029; 50-210.  
 CC SWISS-2DPAGE, P99029; MOUSE.  
 CC Ensembl, ENSMUSG0000024953; Mus musculus.  
 CC MGI, MGI:1859821; Prdx5.  
 CC GO, GO:0005739; Cytochrome; IDA.  
 CC InterPro, IPR000866; Ahpc-TSA.  
 CC InterPro, IPR012336; Thioredoxin-like.  
 CC InterPro, IPR012335; Thioredoxin\_fold.  
 CC Pfam, PF00578; Ahpc-TSA; 1.  
 CC Alternative initiation; Antioxidant; Direct protein sequencing;  
 CC Mitochondrion; Oxidoreductase; Peroxisome; Peroxisome;  
 CC Redox-active center; Transit peptide.  
 CC TRANSIT 1 Mitochondrion (potentia).  
 CC INIT MET 49 49 For isoform Cytoplasmic+peroxisomal.  
 CC CHAIN 50 210 Peroxiredoxin 5, isoform  
 CC Cytoplasmic+peroxisomal.  
 CC FT CHAIN ? 210 Peroxiredoxin 5, isoform Mitochondrial.

FT MOTIF 208 210 Microbody targeting signal (By  
 FT DISULFD 96 200 similarity).  
 FT CONFLICT 55 55 Redox-active (By similarity).  
 FT CONFLICT 83 102 G->D (in Ref. 7).  
 FT GULFGVGAFTPGCKSKTHLP -> VFLCLESIGHLHVLVR  
 FT TA (in Ref. 4).  
 SQ SEQUENCE 210 AA; 21897 MW; E944104CC468BD8 CRC64;  
 Query Match 92.4%; Score 767; DB 1; Length 210;  
 Best local similarity 91.4%; Pred. No. 3.8e-60;  
 Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MAPIKVDPAIPAVEFEGEPGNKNVLAELFKKKGVLPVGAFTPGCKSKTHLPVYQA 60  
 DB 49 MAPIKVDPAIPAVEFEGEPGNKNVLAELFKKKGVLPVGAFTPGCKSKTHLPVYQA 108  
 QY 61 EALRAKGVAVACISVNDAPFTGWSGAHRAKGVRLAPPTGAFGETDLLDDISVSI 120  
 DB 109 GALRAKGVAVACISVNDAPFTGWSGAHRAKGVRLAPPTGAFGETDLLDDISVSI 168  
 QY 121 FGNRLKRFSPVVDGIVKALNVBPDGTLGTLCSLAPNIIISQL 162  
 DB 169 FGNRLKRFSPVVDGIVKALNVBPDGTLGTLCSLAPNIIISQL 210  
 RESULT 6  
 PRDX5\_RAT STANDARD, PRT, 213 AA.  
 ID PRDX5\_RAT STANDARD, PRT, 213 AA.  
 AC Q9R063;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peroxiredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Pxx-V)  
 DE (Peroxisomal antioxidant enzyme) (PLP) (Thioredoxin reductase)  
 DE (Thioredoxin peroxidase PME20) (Antioxidant enzyme B166) (AOB166).  
 GN Name=Prdx5;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=99452929; PubMed=10521424; DOI=10.1074/jbc.274.43.30451;  
 RA Knoops B., Clippe A., Bogard C., Arselane K., Wattiez R., Hermans C.,  
 RA Duconseille E., Falmagne P., Bernard A.,  
 RT "Cloning and characterization of AOB166, a novel mammalian  
 RT antioxidant enzyme of the peroxiredoxin family.";  
 RL J. Biol. Chem. 274:30451-30458(1999).  
 CC -1- FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with  
 CC reducing equivalents provided through the thioredoxin system.  
 CC Involved in intracellular redox signaling (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic  
 CC (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative Initiation;  
 CC Comment=2 isoforms, Mitochondrial (shown here) and  
 CC Cytoplasmic+peroxisomal, are produced by alternative initiation;  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL, AF110732; AAF03751.1; -; mRNA.  
 CC HSSP, P30044; 1HD2.  
 CC SMR, Q9R063; 53-213.  
 CC Ensembl, ENSRNOG0000021125; Rattus norvegicus.



SQ SEQUENCE 162 AA; 17324 MW; 8C6F98D1FA3B74D5 CRC64;

Query Match 91.7%; Score 761; DB 2; Length 162;  
 Best Local Similarity 90.7%; Pred. No. 9.7e-60;  
 Matches 147; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAPIKGDALPAVEVEGEPEGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGEVVEQA 60  
 DB 1 MAPIKGDALPISVVEVEGEPEGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGEVVEQA 60

QY 61 EALKAGVQVVAACLVNDVAFVTGEMGRANRKEGKRLADPTGAFGKETDILLDDSLVSI 120  
 DB 61 EALKAGVQVVAACLVNDVAFVTGEMGRANRKEGKRLADPTGAFGKETDILLDDSLVSI 120

QY 121 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 162  
 DB 121 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 162

RESULT 9  
 PRODX5\_BOVIN STANDARD; PRT; 219 AA.

ID PRODX5\_BOVIN STANDARD; PRT; 219 AA.

AC 09BGI1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Peroxisredoxin 5, mitochondrial precursor (BC 1.11.1.15) (Prx-V)  
 DE (Thioredoxin reductase).  
 GN Name=PRODX5;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 NC NCB1\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Leyens G., Donay I., Knoops B.;  
 RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete  
 peroxiredoxin family in different bovine tissues.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBS databases.  
 CC FUNCTION: Reduces hydrogen peroxide and alkyl hydroperoxides with  
 reducing equivalents provided through the thioredoxin system.  
 CC Involved in intracellular redox signaling (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial, peroxisomal and cytoplasmic  
 (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, Mitochondrial (shown here) and  
 Cytoplasmic-peroxisomal, are produced by alternative initiation;  
 CC -1- SIMILARITY: Belongs to the peroxiredoxin 2 family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

CC EMBL; AF305564; AAG53661.1; -; mRNA.  
 CC HSSP; Q30044; 1HD2.  
 CC SMR; Q9BG11; 59-219.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thioredoxin-like.  
 DR InterPro; IPR012335; Thioredoxin\_fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KM Alternative initiation; Antioxidant; Mitochondrion; Oxidoreductase;  
 KM Peroxisome; Peroxisome; Redox-active center; Transist peptide.  
 FT TRANSIT 1 ? Mitochondrion (potential).  
 FT INIT MET 58 58 For isoform Cytoplasmic+peroxisomal.  
 FT CHAIN 59 219 Cytoplasmic+peroxisomal.

FT CHAIN ? 219 Peroxisredoxin 5, isoform Mitochondrial.  
 FT MOTIF 217 219 Microbody targeting signal (By  
 FT DISULFID 105 209 similarity). (By similarity).  
 SQ SEQUENCE 219 AA; 23211 MW; 93C9B5D794A71581 CRC64;

Query Match 90.0%; Score 747; DB 1; Length 219;  
 Best Local Similarity 87.0%; Pred. No. 2.4e-58;  
 Matches 141; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAPIKGDALPAVEVEGEPEGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGEVVEQA 60  
 DB 58 MAPIKGDALPISVVEVEGEPEGNKVNLAELFKGKGVLPFGPAGFTPGCSKTHLPGEVVEQA 117

QY 61 EALKAGVQVVAACLVNDVAFVTGEMGRANRKEGKRLADPTGAFGKETDILLDDSLVSI 120  
 DB 61 EALKAGVQVVAACLVNDVAFVTGEMGRANRKEGKRLADPTGAFGKETDILLDDSLVSI 120

QY 121 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 162  
 DB 121 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 162

QY 178 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 219  
 DB 178 FGNRLKRFPSMVVDGIVKALNVEBPGTGLTCSLAPNIIISQL 219

RESULT 10  
 Q9D6X2\_MOUSE PRELIMINARY; PRT; 211 AA.

ID Q9D6X2\_MOUSE PRELIMINARY; PRT; 211 AA.

AC Q9D6X2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
 DE library, clone:2310046N07 product:peroxiredoxin 6, full insert  
 DE sequence.  
 GN Name=Prodx5;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaubkawa T., Saito K.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsumoto Y., Niki K., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Oikawa T., Furuno M., Aono H., Balarelli R., Barsh G.,  
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaitanaris M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Taya K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;

RA The FANTOM Consortium.  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team.  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs." ;  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes." ;  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitsumi T., Taahito H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer." ;  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 DR EMBL; AK009858; BAB26548.1; -; mRNA.  
 DR HSSP; P30044; 1HD2.  
 DR SMR; Q9D6X2; 54-211.  
 DR Ensembl; ENSMUSG0000024953; Mus musculus.  
 DR MGI; MGI:1859821; Ptdx5.  
 DR GO; GO:0005739; C:mitochondrion; IDA.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thiorodoxin-like.  
 DR InterPro; IPR012335; Thiorodoxin-fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
 SQ SEQUENCE 211 AA; 22500 MW; 676B09BCE10098 CRC64;  
 QY Query Match 87.6%; Score 727; DB 2; Length 211;  
 DB Best Local Similarity 89.2%; Pred. No. 1.4e-56;  
 DB Matches 111; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
 QY 5 KVGDAIPAVEVFEGEPGNKVNIALFPGKGGVLFVGGAFTPGCSKTHLPGFYQAQAL 64  
 DB 54 KVGDAIPAVEVFEGEPGNKVNIALFPGKGGVLFVGGAFTPGCSKTHLPGFYQAQAL 113  
 QY 65 AKGVQVAVACLVNDADVTGEMGPAHKAEGKVRLLAPPTAGFGEPTLLDDSVITGNR 124  
 DB 114 AKGAQVAVACLVNDADVTGEMGPAHKAEGKVRLLAPPTAGFGEPTLLDDSVITGNR 173  
 QY 125 RLKRFNVVODGIVKLVNVEPDTGLTCSLAPNIISQL 162  
 DB 174 RLKRFNVVODGIVKLVNVEPDTGLTCSLAPNIISQL 211

RESULT 11  
 Q6GPY3\_XENLA PRELIMINARY; PRT; 189 AA.  
 AC Q6GPY3;  
 DT 05-JUL-2004 (TRMBLrel. 27, Created)  
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)  
 DE MGCS2521 protein.  
 GN Name=MGCS2521;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OC NCBI\_Taxid=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalski V., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=2241132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative." ;  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX Klein S., Gerhard D.S.;  
 RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
 DR EMBL; BC072972; AAH72972.1; -; mRNA.  
 DR SMR; Q6GPY3; 30-189.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0004601; F:peroxidase activity; IEA.  
 DR InterPro; IPR000866; Ahpc-TSA.  
 DR InterPro; IPR012336; Thiorodoxin-like.  
 DR InterPro; IPR012335; Thiorodoxin-fold.  
 DR Pfam; PF00578; Ahpc-TSA; 1.  
 KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
 SQ SEQUENCE 189 AA; 20066 MW; 5EA78C7EBD24D808 CRC64;  
 QY Query Match 70.3%; Score 583.5; DB 2; Length 189;  
 DB Best Local Similarity 70.0%; Pred. No. 7.3e-44;  
 DB Matches 112; Conservative 17; Mismatches 30; Indels 1; Gaps 1;  
 QY 4 IKVGAIPAVEVFEGEPGNKVNIALFPGKGGVLFVGGAFTPGCSKTHLPGFYQAQAL 63  
 DB 30 IKVGAIPAVEVFEGEPGNKVNIALFPGKGGVLFVGGAFTPGCSKTHLPGFYQAQAL 89

QY 64 KAKGVAVACLSVNDVAFVTGEMGRHAKRAEGRVRLADPTGAFGKETDLDLDDSLVSIIFG 122  
 DB 90 KSRGAAVACLSVNDVAFVTGEMGRHAKRAEGRVRLADPTGAFGKETDLDLDDSLVSIIFG 149  
 QY 123 NRRLKPSMVVODGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 DB 150 NQRCRFSMVVEDGKIKALNVEPDGTGLTCSLAPNIISQL 189

## RESULT 12

Q502C8 BRABE PRELIMINARY; PRT; 162 AA.  
 ID Q502C8; BRABE PRELIMINARY; PRT; 162 AA.  
 AC Q502C8;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein zgc:112318.  
 GN ORFNames=zgc:112318;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 CC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheaf C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dichtenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalski U., Smallos D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA NIH MGC Project;  
 RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2O) + ROH.  
 DR EMBL; BC095755; AAH95755.1; -; mRNA.  
 DR Ensemble; ENSDARG0000020317; Danio rerio.  
 DR ZFIN; ZDB-GENE-050522-159; zgc:112318.  
 DR InterPro; IPR000866; AhpC-TSA.  
 DR InterPro; IPR012336; Thioresoxin-like.  
 DR InterPro; IPR012335; Thioresoxin-fold.  
 DR Pfam; PF00578; AhpC-TSA; 1.  
 DR Antioxidant; Hypothetical protein; Oxidoreductase; Peroxidase;  
 KW Redox-active center.  
 SQ SEQUENCE 162 AA; 17109 MW; 5C7C1CE753E0B41 CRC64;

Query Match 64.6%; Score 536.5; DB 2; Length 162;  
 Best Local Similarity 60.9%; Pred. No. 9,4e-40;  
 Matches 98; Conservative 33; Mismatches 29; Indels 1; Gaps 1;

QY 3 PIKVGDAIPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFTRPGCKSTHLPGEVQAEA 62  
 DB 2 PIKVGQRLPAVVOEDPNSISMELSCRRGVLFVPGATTPGCKSTHLPGEVQAGE 61  
 QY 63 LKAGVQVAVACLSVNDVAFVTGEMGRHAKRAEGRVRLADPTGAFGKETDLDLDDSLVSIIF 121

DB 62 LKAGVEVAVACLSVNDVAFVMSAMGKQNGADGKVMADPTGAFTRKAVDLVLMNAQLIPVL 121  
 QY 122 GNRLKPSMVVODGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 DB 122 GNLRQRYAMLIENGAVTKLSVEPDGTGLTCSLAPNIISQL 162

## RESULT 13

Q8T5Q7 BRABE PRELIMINARY; PRT; 188 AA.  
 ID Q8T5Q7; BRABE PRELIMINARY; PRT; 188 AA.  
 AC Q8T5Q7;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Peroxisome oxidin V protein.  
 GN Name=AmpHixV;  
 OS Branchiostoma belcheri tsingtauense.  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 CC Branchiostoma.  
 OX NCBI\_TaxID=155462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zhang S., Liu Z., Yuan J., Liu M., Wei J., Xu A.,  
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2O) + ROH.  
 DR EMBL; AF498232; AAM18076.1; -; mRNA.  
 DR HSSP; P30044; IHD2.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0004601; F:peroxidase activity; IEA.  
 DR InterPro; IPR000866; AhpC-TSA.  
 DR InterPro; IPR012336; Thioresoxin-like.  
 DR InterPro; IPR012335; Thioresoxin-fold.  
 DR Pfam; PF00578; AhpC-TSA; 1.  
 DR Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
 KW Antioxidant; 19802 MW; 3FCB6C23AA0B2726 CRC64;  
 SQ SEQUENCE 188 AA; 19802 MW; 3FCB6C23AA0B2726 CRC64;

Query Match 63.1%; Score 524; DB 2; Length 188;  
 Best Local Similarity 65.4%; Pred. No. 1.4e-38;  
 Matches 102; Conservative 18; Mismatches 34; Indels 2; Gaps 1;

QY 3 PIKVGDAIPAVEVEGEBGNKVNLAELFKGKKGVLFVPGAFTRPGCKSTHLPGEVQAEA 62  
 DB 33 PIKVGDKLPGDILENTPGNVNVSELPAGKKGVLFVPGAFTRPGCKSTHLPGEVQAKGD 92  
 QY 63 LKAGVQVAVACLSVNDVAFVTGEMGRHAKRAEGRVRLADPTGAFGKETDLDLDDSLVSIIF 122  
 DB 93 LKAGVQVAVACLSVNDVAFVTGEMGRHAKRAEGRVRLADPTGAFGKETDLDLDDSLVSIIF 150  
 QY 123 NRRLKPSMVVODGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 DB 151 NIKSRYSMLVEDGKQALNVEPDGTGLTCSLAPNIISQL 186

## RESULT 14

Q5UG08 AEDAE PRELIMINARY; PRT; 157 AA.  
 ID Q5UG08; AEDAE PRELIMINARY; PRT; 157 AA.  
 AC Q5UG08;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE Peroxisome oxidin V protein.  
 GN Aedes aegypti (Yellow fever mosquito).  
 OS Aedes aegypti (Yellow fever mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;  
 CC Culicinae; Culicini; Aedes; Stegomyia.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Tissue=Salivary gland;  
 RA Chandra P.K., Wikel S.K.,  
 RT "Complementing the stamome of the adult female Aedes aegypti  
 mosquito.";

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Conjugation of reduced glutathione to a wide number of  
CC exogenous and endogenous hydrophobic electrophiles (By  
CC similarity).  
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
CC -!- SUBUNIT: Homodimer (By similarity).  
DR EMBL; AY738253; AAV4853.1; -; mRNA.  
DR GO; GO:0016491; P:oxidoreductase activity; IEA.  
DR GO; GO:0004601; F:peroxidase activity; IEA.  
DR InterPro; IPR000866; Ahpc-TSA.  
DR InterPro; IPR012336; Thiooxidin-like.  
DR InterPro; IPR012335; Thiooxidin\_fold.  
DR Pfam; PF00578; Ahpc-TSA; 1.  
KW Antioxidant; Oxidoreductase; Peroxidase; Redox-active center.  
SQ SEQUENCE 157 AA; 16644 MW; 02B974DB7723DBE6 CRC64;

Query Match 59.6%; Score 494.5; DB 2; Length 157;  
Best Local Similarity 58.2%; Pred. No. 5e-36;  
Matches 92; Conservative 26; Mismatches 37; Indels 3; Gaps 1;

QY 1 MAPIKVGDALPAVEVEGEGRNKVNLAELFKGKGVLFVPGAFPPGCKTHLPGFVEQA 60  
DB 1 MVQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLFVPGAFPPGCKTHLPGVNDRA 60  
QY 61 EALKAKGVQVAVCLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDLSVSI 120  
DB 61 DAIKSSGVEICVSVNDPFWMSAWGKQHNATGKVRMLADPAALFTKQLELGD--LPP 117  
QY 121 FGNRLKRFPSMWVODGIVKALNVEPDGTGLTCSLAPNI 158  
DB 118 LGILRSKRYSMVLBDGVKSLNVEPDGTGLSCSLADKI 155

RESULT 15  
Q7PUM1\_ANOGA  
ID Q7PUM1 ANOGA PRELIMINARY; PRT; 246 AA.  
AC Q7PUM1;  
DT 01-MAR-2004 (Tremblrel. 26, Created)  
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE ENSANGP0000020393 (Fragment).  
GN ORFNames=ENSANG00000017904;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematoceera; Culicoidae; Culicidae;  
OC Anophelinae; Anopheles.  
OK NCBI\_TaxId=180454;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST.  
RA Anopheles Genome Sequencing Consortium.  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -!- CATALYTIC ACTIVITY: 2 R'-SH + ROOH = R'-S-S-R' + H(2)O + ROH.  
DR EMBL; AAB01008987; EAA01313.2; -; Genomic\_DNA.  
DR HSSP; P30044; 1HD2.  
DR GO; GO:0016209; F:antioxidant activity; IEA.  
DR InterPro; IPR000866; Ahpc-TSA.  
DR InterPro; IPR012336; Thiooxidin-like.  
DR InterPro; IPR012335; Thiooxidin\_fold.  
DR Pfam; PF00578; Ahpc-TSA; 1.  
KW Antioxidant.  
FT NON\_TER 1  
SQ SEQUENCE 246 AA; 26218 MW; 4CACCB3F50C8E2A3 CRC64;

Query Match 58.6%; Score 486.5; DB 2; Length 246;  
Best Local Similarity 58.9%; Pred. No. 4.2e-35;  
Matches 93; Conservative 22; Mismatches 40; Indels 3; Gaps 1;

QY 1 MAPIKVGDALPAVEVEGEGRNKVNLAELFKGKGVLFVPGAFPPGCKTHLPGFVEQA 60  
DB 1 MVQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLFVPGAFPPGCKTHLPGVNDRA 60  
QY 61 EALKAKGVQVAVCLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDLSVSI 120  
DB 61 DAIKSSGVEICVSVNDPFWMSAWGKQHNATGKVRMLADPAALFTKQLELGD--LPP 117  
QY 121 FGNRLKRFPSMWVODGIVKALNVEPDGTGLTCSLAPNI 158  
DB 118 LGILRSKRYSMVLBDGVKSLNVEPDGTGLSCSLADKI 155

DB 90 MVQIKEGDKIPSIDLFEDSPANKVMADLCAGKVVLFVPGAFPPGCKTHLPGFVEKA 149  
QY 61 EALKAKGVQVAVCLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDLSVSI 120  
DB 150 GDLKSSGATEICVSVNDPFWMSAWGKQHNATGKVRMLADPAALFTKQLELGD--LPP 206  
QY 121 FGNRLKRFPSMWVODGIVKALNVEPDGTGLTCSLAPNI 158  
DB 207 LGILRSKRYSMVLBDGVKSLNVEPDGTGLSCSLADKI 244

Search completed: February 21, 2006, 21:46:11  
Job time : 234 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:57:41 ; Search time 168 Seconds  
(without alignments)  
402.907 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPKVGDAIPAVEFEGEP.....YEDPOTGLTCSLAPNIIISQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA Main:

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	830	100.0	162	US-10-408-765A-2152	Sequence 2152, App1
2	830	100.0	162	US-10-686-157-2	Sequence 2, App1
3	830	100.0	205	US-10-276-774-1773	Sequence 1773, App1
4	830	100.0	214	US-10-394-116-1	Sequence 1, App1
5	830	100.0	214	US-10-408-765A-770	Sequence 770, App1
6	830	100.0	214	US-10-974-148-20	Sequence 20, App1
7	830	100.0	214	US-10-686-157-21	Sequence 21, App1
8	825	99.4	161	US-10-408-765A-2397	Sequence 2397, App1
9	777	99.6	226	US-10-264-049-3514	Sequence 3514, App1
10	767	99.4	162	US-10-686-157-6	Sequence 6, App1
11	752	99.6	162	US-10-686-157-4	Sequence 4, App1
12	747	99.0	219	US-10-732-923-21551	Sequence 21551, App1
13	725	87.3	217	US-10-424-599-246448	Sequence 246448, App1
14	667	80.4	150	US-10-263-828-97	Sequence 97, App1
15	573	69.0	169	US-10-491-183-16	Sequence 16, App1
16	569	68.6	351	US-10-450-763-51040	Sequence 51040, App1
17	524	63.1	188	US-10-732-923-21448	Sequence 21448, App1
18	498	60.0	137	US-10-972-024-470	Sequence 470, App1
19	481	58.0	190	US-10-732-923-21547	Sequence 21547, App1
20	479	57.7	157	US-11-097-143-16080	Sequence 16080, App1
21	476.5	57.4	153	US-10-732-923-21451	Sequence 21451, App1
22	475.5	57.3	175	US-10-732-923-21450	Sequence 21450, App1
23	469.5	56.6	285	US-10-450-763-39760	Sequence 39760, App1
24	400.5	48.3	185	US-10-732-923-21545	Sequence 21545, App1
25	349	42.0	125	US-10-972-024-178	Sequence 178, App1
26	346	41.7	130	US-10-264-049-3474	Sequence 3474, App1
27	332	40.0	183	US-10-767-701-51758	Sequence 51758, App1

28	317	38.2	161	5	US-10-732-923-21458	Sequence 21458, A
29	317	38.2	191	5	US-10-732-923-21466	Sequence 21466, A
30	313.5	37.8	202	5	US-10-732-923-21447	Sequence 21447, A
31	312.5	37.7	160	5	US-10-732-923-21456	Sequence 21456, A
32	310.5	37.4	163	5	US-10-732-923-21462	Sequence 21462, A
33	310.5	37.4	160	5	US-10-732-923-21518	Sequence 21518, A
34	310.5	37.3	162	4	US-10-310-154-687	Sequence 687, App1
35	310	37.3	162	5	US-10-732-923-21516	Sequence 21516, A
36	310	37.3	162	5	US-10-732-923-21517	Sequence 21517, A
37	310	37.3	215	4	US-10-424-599-244213	Sequence 244213, A
38	310	37.3	248	4	US-10-425-114-51447	Sequence 51447, A
39	310	37.3	249	5	US-10-732-923-21493	Sequence 21493, A
40	309.5	37.3	159	5	US-10-732-923-21527	Sequence 21527, A
41	308.5	37.2	196	5	US-10-732-923-21534	Sequence 21534, A
42	308	37.1	157	5	US-10-732-923-21463	Sequence 21463, A
43	306	36.9	162	4	US-10-424-599-257249	Sequence 257249, A
44	305	36.7	158	5	US-10-732-923-21460	Sequence 21460, A
45	303	36.5	161	5	US-10-732-923-21453	Sequence 21453, A

## ALIGNMENTS

```

RESULT 1
US-10-408-765A-2152
; Sequence 2152, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2152
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2152

Query Match      100.0%; Score 830; DB 4; Length 162;
Best local similarity 100.0%; Pred. No. 4.8e-65;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAPKVGDAIPAVEFEGEPGNKYNLAELFGKKGVLFVGAFPTGCGSKTHLPQFYQA 60
        |||
DB       1  MAPKVGDAIPAVEFEGEPGNKYNLAELFGKKGVLFVGAFPTGCGSKTHLPQFYQA 60
        |||

QY      61  EALAKGVQVAAACSVNDAFTTGWGRRAHKEGVRIADPTGAPGKETTLLDLSYIS 120
        |||
DB       61  EALAKGVQVAAACSVNDAFTTGWGRRAHKEGVRIADPTGAPGKETTLLDLSYIS 120
        |||

QY      121  FGNRLKRFMSWVODGVIKALNVEPDGTGLTCSLAPNIIISQL 162
        |||
DB       121  FGNRLKRFMSWVODGVIKALNVEPDGTGLTCSLAPNIIISQL 162
        |||

RESULT 2
US-10-686-157-2
; Sequence 2, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding

```

```

1 TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
2 TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
3 TITLE OF INVENTION: disorders
4 TITLE OF INVENTION:
5 FILE REFERENCE: DECL30.001CPI
6 CURRENT APPLICATION NUMBER: US/10/686,157
7 CURRENT FILING DATE: 2003-10-15
8 PRIOR APPLICATION NUMBER: US 6,759,194
9 PRIOR FILING DATE: 2000-08-15
10 PRIOR APPLICATION NUMBER: PCT/BE98/00124
11 PRIOR FILING DATE: 1998-08-20
12 PRIOR APPLICATION NUMBER: BE 1011331
13 PRIOR FILING DATE: 1997-08-20
14 NUMBER OF SEQ ID NOS: 21
15 SOFTWARE: PatentIn version 3.3
16 SEQ ID NO 2
17 LENGTH: 162
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-10-686-157-2

```

Query Match	100.0%;	Score 830;	DB 5;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 4.8e-85;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MAPKVGDAIPAVEVEGEENKVNIAELFKKKKGLVLCVPEAFPGSGKTHLPGFPEQA	60
Db	1	MAPLKGDALPAVEVEGEPGNKNIAELFKKKKGLVLCVPEAFPGSGKTHLPGFPEQA	60
Qy	61	EALKAKGVQVACLSVNDAFVTGGEWRARAKAGKRVLLADPFGAFGKRTDLLDDSLVSI	120
Db	61	EALKAKGVQVACLSVNDAFVTGGEWRARAKAGKRVLLADPFGAFGKRTDLLDDSLVSI	120
Qy	121	FGNRRLRRFSMVVQDGIIVALKANLEPDSGLTCSLAPNIISQL	162
Db	121	FGNRRLRRFSMVVQDGIIVALKANLEPDSGLTCSLAPNIISQL	162

```

: RESULT 3
: US-10-276-774-1773
: Sequence 1773, Application US/10276774
: Publication No. US20040053245A1
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: APPLICANT: Tang, Y, Tom et al
: TITLE OF INVENTION: 'NO. US20040053245A1 Nucleic Acids and Polypeptides
: FILE REFERENCE: 21272-030
: CURRENT APPLICATION NUMBER: US/10/276, 774
: PRIOR FILING DATE: 2002-11-18
: PRIOR APPLICATION NUMBER: 09/560, 875
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: 09/496, 914
: PRIOR FILING DATE: 2000-02-03
: NUMBER OF SEQ ID NOS: 2700
: SOFTWARE: Custom
: SEQ ID NO 1773
: LENGTH: 205
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-276-774-1773

```

Query Match	100.0%	Score 830	DB 4	Length 205
Best Local Similarity	100.0%	Pred. No. 6.6e-85		
Matches	162	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	MAPIVGVGAIIPAVEVEEGEGPGKNKVNLAELFKKKGGVLPGVPGCAPPGGSKTHLPGFVBOA	60	
Db	44	MAPIVGVGAIIPAVEVEEGEGPGKNKVNLAELFKKKGGVLPGVPGCAPPGGSKTHLPGFVBOA	103	
QY	61	EALKAAGVQVVACTSVNDAFVTVGEMGRARHKEGKRLADPFGAEGKETDILLDDSLYSI	120	
Db	104	EALKAAGVQVVACTSVNDAFVTVGEMGRARHKEGKRLADPFGAEGKETDILLDDSLYSI	163	
QY	121	FGNRLKRFSMVVDGIVKALNVBDDGTGLTCSLAPNIISQL	162	

Db 164 FGNRLKRFMSVQDGIKALNVEPDGTGLTCSLAPNIISQL 205

```

RESULT 4
US-10-394-136-1
Sequence 1, Application US/10394136
Publication No. US20030175787A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: VESICLE MEMBRANE PROTEINS
FILE REFERENCE: PC-0029 CIP
CURRENT APPLICATION NUMBER: US/10/394,136
CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: US/09/718,996
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030175787A1 743725
US-10-394-136-1

```

Query Match	100.0%;	Score 830;	DB 4;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 7e-85;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 5
US-10-408-765A-770
Sequence 770, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boib D.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 770
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-770

```

Query Match 100.0%; Score 830; DB 4; Length 214;

Best Local Similarity 100.0%; Pred. No. 7e-85;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 60  
DB 53 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 112  
QY 61 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 120  
DB 113 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 172  
QY 121 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 162  
DB 173 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 214

## RESULT 6

US-10-974-148-20  
Sequence 20, Application US/10974148  
Publication No. US20050123962A1

## GENERAL INFORMATION:

APPLICANT: Gan, Li  
APPLICANT: Gonzalez-Zulueta, Mirella  
APPLICANT: Ye, Shiming  
APPLICANT: Uferer, Roman  
TITLE OF INVENTION: Regulated Nucleic Acids in Pathogenesis of Alzheimer's Disease  
FILE REFERENCE: AGT-048  
CURRENT APPLICATION NUMBER: US/10/974,148  
CURRENT FILING DATE: 2004-10-26  
PRIOR APPLICATION NUMBER: 60/515,536  
PRIOR FILING DATE: 2003-10-28  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 20  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-974-148-20

Query Match 100.0%; Score 830; DB 5; Length 214;  
Best Local Similarity 100.0%; Pred. No. 7e-85;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 60  
DB 53 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 112  
QY 61 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 120  
DB 113 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 172  
QY 121 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 162  
DB 173 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 214

## RESULT 7

US-10-686-157-21  
Sequence 21, Application US/10686157  
Publication No. US20050142126A1

## GENERAL INFORMATION:

APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN  
APPLICANT: UNIVERSITE DE MONS-HAINAUT  
TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding  
TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment  
TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related  
FILE REFERENCE: DEC130.001CPI  
CURRENT APPLICATION NUMBER: US/10/686,157  
CURRENT FILING DATE: 2003-10-15  
PRIOR APPLICATION NUMBER: US 6,759,194  
PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: PCT/BE98/00124

PRIOR FILING DATE: 1998-08-20

PRIOR APPLICATION NUMBER: BE 1011331

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn version 3.3

SEQ ID NO 21

LENGTH: 214

TYPE: PRT

ORGANISM: Homo sapiens

US-10-686-157-21

Query Match 100.0%; Score 830; DB 5; Length 214;  
Best Local Similarity 100.0%; Pred. No. 7e-85;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 60  
DB 53 MAPIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 112  
QY 61 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 120  
DB 113 EALAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 172  
QY 121 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 162  
DB 173 FGNRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 214

## RESULT 8

US-10-408-765A-2397  
Sequence 2397, Application US/10408765A  
Publication No. US20040101874A1

## GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Fahy, Eoin D.  
APPLICANT: Zhang, Bing  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary M.  
APPLICANT: Warnock, Dale E.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
FILE REFERENCE: 660088.465  
CURRENT APPLICATION NUMBER: US/10/408,765A  
CURRENT FILING DATE: 2003-04-04  
NUMBER OF SEQ ID NOS: 3077  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2397  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-408-765A-2397

Query Match 99.4%; Score 825; DB 4; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.7e-84;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 61  
DB 1 APIKVGDAIPAVEFESEPGNKVNLAELFKGKGVLFVPGATTPGCSKTHLPFVEQA 60  
QY 62 ALKAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 121  
DB 61 ALKAKGVQVVAACSVNDAFTGEMGRHAKAGKVRLLADPTGAFGKETDILLDSLSVI 120  
QY 122 GNRRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 162  
DB 121 GNRRLKRFMSVWVDGIVKALNVEBDGTGTCSLAPNIISQL 161

## RESULT 9

US-10-264-049-3514

```

; Sequence 3514, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3514
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (79)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (90)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (190)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (225)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3514

Query Match          93.6%; Score 777; DB 4; Length 226;
Best Local Similarity 95.1%; Pred. No. 7,1e-79;
Matches 154; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  MAPIVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60
      |||
DB      52  MAPIVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 111
      |||

QY      61  EALKKAGVVAVACISVNDAPFTGEMGRARAKAGKRVRLADPTGARGKETDILLDSLVSI 120
      |||
DB      112  EALKKAGVVAVACISVNDAPFTGEMGRARAKAGKRVRLADPTGARGKETDILLDSLVSI 171
      |||

QY      121  FGNRLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
      |||
DB      172  FGNRLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIISOL 213
      |||

RESULT 10
US-10-686-157-6
; Sequence 6, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: Peroxisome-associated polypeptide, nucleotide sequence encoding
```

```

; TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
; TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
; FILE REFERENCE: DECLE30.001CPI
; CURRENT APPLICATION NUMBER: US/10/686,157
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 6,759,194
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: PCT/BE98/00124
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: BE 1011331
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-686-157-6

Query Match          92.4%; Score 767; DB 5; Length 162;
Best Local Similarity 91.4%; Pred. No. 6,1e-78;
Matches 148; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      1  MAPIVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60
      |||
DB      1  MAPIVGDAIPAVEVEFEGEPGNKVNLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60
      |||

QY      61  EALKKAGVVAVACISVNDAPFTGEMGRARAKAGKRVRLADPTGARGKETDILLDSLVSI 120
      |||
DB      61  EALKKAGVVAVACISVNDAPFTGEMGRARAKAGKRVRLADPTGARGKETDILLDSLVSI 120
      |||

QY      121  FGNRLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
      |||
DB      121  FGNRLKRFPSMVVODGIVKALNVEPDGTGLTCSLAPNIISOL 162
      |||

RESULT 11
US-10-686-157-4
; Sequence 4, Application US/10686157
; Publication No. US20050142126A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
; APPLICANT: UNIVERSITE DE MONS-HAINAUT
; TITLE OF INVENTION: said polypeptide and their uses in the diagnosis and/or treatment
; TITLE OF INVENTION: of lung injuries and diseases, and of oxidative stress-related
; FILE REFERENCE: DECLE30.001CPI
; CURRENT APPLICATION NUMBER: US/10/686,157
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 6,759,194
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: PCT/BE98/00124
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: BE 1011331
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Rattus rattus
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X = E or G
; NAME/KEY: MISC_FEATURE
; LOCATION: (63)..(63)
; OTHER INFORMATION: X = L or P
; FEATURE:
; NAME/KEY: MISC_FEATURE
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LOCATION: (79)..(79)  
OTHER INFORMATION: X = L or P  
US-10-686-157-4

Query Match 90.6%; Score 752; DB 5; Length 162;  
Best Local Similarity 88.9%; Pred. No. 3e-76;  
Matches 144; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 60  
DB 1 MAPIKVGDTIPSVVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 60  
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
DB 61 GAXAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
QY 121 FGNRLKRFMSNVODGIVKALNVEPDGTGTCSLAPNIIISQL 162  
DB 121 FGNRLKRFMSNVIDKGVKALNVEPDGTGTCSLAPNIIISQL 162

## RESULT 12

US-10-732-923-21551  
Sequence 21551, Application US/10732923  
Publication No. US20050108791A1  
GENERAL INFORMATION:  
APPLICANT: Edgerton, Michael D  
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
FILE REFERENCE: 38-15(52796)C  
CURRENT APPLICATION NUMBER: US/10/732,923  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: 10/310,154  
PRIOR FILING DATE: 2002-12-04  
NUMBER OF SEQ ID NOS: 24149  
SEQ ID NO 21551  
LENGTH: 219  
TYPE: PRT  
ORGANISM: Bos taurus  
US-10-732-923-21551

Query Match 90.0%; Score 747; DB 5; Length 219;  
Best Local Similarity 87.0%; Pred. No. 1.6e-75;  
Matches 141; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 60  
DB 58 MAPIKVGDAIPSVVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 117  
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
DB 118 DALAKGVQVAVCLTVNDVFTBEMARHKAEGKVRLLADPSGTFGKETDILLDDSLVSI 177  
QY 121 FGNRLKRFMSNVODGIVKALNVEPDGTGTCSLAPNIIISQL 162  
DB 178 FGNRLKRFMSNVIEDGIVKSLNVEPDGTGTCSLAPNIIISQL 219

## RESULT 13

US-10-424-599-246448  
Sequence 246448, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 246448

LENGTH: 217

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure  
LOCATION: (1)..(217)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_64574C.1 pep  
US-10-424-599-246448

Query Match 87.3%; Score 725; DB 4; Length 217;  
Best Local Similarity 86.4%; Pred. No. 4.9e-73;  
Matches 140; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 60  
DB 53 MAPIKVGDTIPSVVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 112  
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
DB 113 GALAKGVQVAVCLSVNDAFVTADMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172  
QY 121 FGNRLKRFMSNVODGIVKALNVEPDGTGTCSLAPNIIISQL 162  
DB 173 FGNRLKRFMSNVIDKGVKALNVEPDGTGTCSLAPNIIISQL 214

## RESULT 14

US-10-263-828-97  
Sequence 97, Application US/10263828  
Publication No. US20030138905A1  
GENERAL INFORMATION:  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Glenn, Matthew  
APPLICANT: Grigor, Murray R.  
APPLICANT: Molenaar, Adrian J.  
TITLE OF INVENTION: Compositions isolated from bovine  
TITLE OF INVENTION: mammary gland and methods for their use.  
FILE REFERENCE: 11000.10440icon  
CURRENT APPLICATION NUMBER: US/10/263,828  
CURRENT FILING DATE: 2002-10-02  
NUMBER OF SEQ ID NOS: 136  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97  
LENGTH: 150  
TYPE: PRT  
ORGANISM: Bovine  
US-10-263-828-97

Query Match 80.4%; Score 667; DB 4; Length 150;  
Best Local Similarity 87.0%; Pred. No. 1e-66;  
Matches 127; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 60  
DB 5 MAPIKVGDAIPSVVEFEGEPGNKVNLAELFKGKGVLFVGVGAFPPGCKTHLPGFVQA 64  
QY 61 EALAKGVQVAVCLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
DB 65 DALAKGVQVAVCLTVNDVFTBEMARHKAEGKVRLLADPSGTFGKETDILLDDSLVSI 124  
QY 121 FGNRLKRFMSNVODGIVKALNVEPD 146  
DB 125 FGNRLKRFMSNVIEDGIVKSLNVEPD 150

## RESULT 15

US-10-491-183-16  
Sequence 16, Application US/10491183  
Publication No. US20050191627A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE CORPORATION; YANG, Junming

```

; APPLICANT: LU, Dyrung, Alina M.; YUE, Henry
; APPLICANT: ELIOT, Vicki S.; WARREN, Bridget A.
; APPLICANT: DUGAN, Brendan M.; FORSYTHE, Ian J. A.
; APPLICANT: LEE, Ernestine A.; HAPALIA, April J. A.
; APPLICANT: RAMKUMAR, Jayalakmi; CHAMLA, Nandinder K.
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.
; APPLICANT: GORVAD, Ann E.; TRAN, Uyen K.
; APPLICANT: LI, Joana X.; YAO, Monique G.
; APPLICANT: ISON, Craig H.; GRIFFIN, Jennifer A.
; APPLICANT: LEE, Soo Yeun; CHANG, Hei-n-Ru
; APPLICANT: EMERLING, Brooke M.; TANG, Y. Tom
; APPLICANT: LAL, Preeti G.; KABLE, Amy E.
; APPLICANT: MARQUIS, Joseph P.; JIANG, Xin
; APPLICANT: JACKSON, Alan A.; ZEBARJADIAN, Yeganeh
; APPLICANT: SWARNAKAR, Anita; WILSON, Amy D.
; APPLICANT: JIN, Pei; RICHARDSON, Thomas W.
; APPLICANT: BHATIA, Umesh; BURRILL, John D.
; APPLICANT: LEE, Sally; BLAKE, Julie J.
; APPLICANT: HO, Anne; ZHENG, Wenjin
; APPLICANT: GAO, Jing
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1214 USN
; CURRENT APPLICATION NUMBER: US/10/491,183
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/US02/31096
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,388
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/328,979
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/346,034
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/348,284
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/338,048
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/332,340
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/387,119
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 169
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7500495CD1
; US-10-491-183-16

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Query Match          69.0%; Score 573; DB 5; Length 169;
Best Local Similarity 100.0%; Pred. 4.7e-56;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 50 KTHLPGFVQABALAKAGVAVACLSVNDAPVYTGEMGRAHAKAGKVRLLADPTGAFGKET 109
DB 57 KTHLPGFVQABALAKAGVAVACLSVNDAPVYTGEMGRAHAKAGKVRLLADPTGAFGKET 116
QY 110 DILLDDSLVSIIFGNRLKRFPSNVVDGIVKALNVEPDGTGLTCSLAPNTISQL 162
DB 117 DILLDDSLVSIIFGNRLKRFPSNVVDGIVKALNVEPDGTGLTCSLAPNTISQL 169

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Search completed: February 21, 2006, 22:00:57  
 UOB time : 169 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:58:17 ; Search time 18 Seconds  
(without alignments)

128.157 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830  
Sequence: 1 MAPKVGDAIPAVEVEFEGEP.....VEPDGTGLTCSLAPNIIISQL 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 108093 seqs, 14239677 residues

Total number of hits satisfying chosen parameters: 108093

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PC7\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	214	6	US-10-878-556A-183 Sequence 183, App
2	252.5	30.4	267	6	US-10-467-657-5556 Sequence 5556, Ap
3	107	12.9	187	7	US-11-058-926-22 Sequence 22, Appl
4	97	11.7	188	7	US-11-058-926-24 Sequence 24, Appl
5	96	11.6	271	6	US-10-821-234-1419 Sequence 1419, Ap
6	90.5	10.9	257	6	US-10-642-272A-6 Sequence 6, Appl1
7	89.5	10.8	206	6	US-10-642-272A-4 Sequence 4, Appl1
8	89	10.7	257	6	US-10-821-234-1038 Sequence 1038, Ap
9	86.5	10.4	257	6	US-10-642-272A-5 Sequence 5, Appl1
10	86	10.4	198	6	US-10-642-272A-28 Sequence 28, Appl
11	81	9.8	386	6	US-10-467-657-6564 Sequence 6564, Ap
12	79	9.5	193	6	US-10-527-771-6 Sequence 6, Appl1
13	78.5	9.5	442	6	US-10-485-788A-516 Sequence 516, App
14	78.5	9.5	724	7	US-11-126-313-28 Sequence 28, Appl
15	78.5	9.5	1219	7	US-11-032-236-4 Sequence 4, Appl1
16	77.5	9.3	446	7	US-11-108-172-1121 Sequence 1121, Ap
17	76	9.2	1170	6	US-10-858-730-71 Sequence 71, Appl
18	75	9.0	105	6	US-10-485-788A-794 Sequence 794, App
19	75	9.0	1495	7	US-11-053-076-176 Sequence 176, App
20	74.5	9.0	1095	7	US-11-019-711-111 Sequence 111, App
21	74	8.9	1588	7	US-11-052-554A-280 Sequence 280, App
22	71	8.6	164	6	US-10-793-626-252 Sequence 252, App
23	70.5	8.5	3507	7	US-11-075-185-7 Sequence 7, Appl1
24	69.5	8.4	7968	7	US-11-143-980-49 Sequence 49, Appl
25	69	8.3	621	7	US-11-098-686-10946 Sequence 10946, A

26	69	8.3	1479	7	US-11-019-711-36 Sequence 36, Appl
27	69	8.3	4868	7	US-11-044-111-24 Sequence 24, Appl
28	69	8.3	8695	7	US-11-205-109-15 Sequence 15, Appl
29	68.5	8.3	509	7	US-11-098-686-10996 Sequence 10996, A
30	68	8.2	165	6	US-10-454-437-172 Sequence 172, App
31	68	8.2	1571	7	US-11-052-554A-2 Sequence 2, Appl
32	68	8.2	7102	7	US-11-143-980-48 Sequence 48, Appl
33	67.5	8.1	365	6	US-10-454-437-394 Sequence 394, App
34	67	8.1	4060	6	US-10-922-232B-55 Sequence 55, Appl
35	67	8.1	6738	6	US-10-922-232B-56 Sequence 56, Appl
36	66.5	8.0	3073	7	US-11-143-980-50 Sequence 50, Appl
37	66.5	8.0	5712	7	US-11-143-980-47 Sequence 47, Appl
38	66	8.0	284	6	US-10-485-517-326 Sequence 326, App
39	66	8.0	371	6	US-10-467-657-1926 Sequence 1926, App
40	65.5	7.9	95	6	US-10-485-788A-659 Sequence 659, App
41	65.5	7.9	95	7	US-11-053-076-22 Sequence 22, Appl
42	65.5	7.9	177	6	US-10-980-388-95 Sequence 95, Appl
43	65.5	7.9	239	7	US-11-194-246-304 Sequence 304, Appl
44	65.5	7.9	257	6	US-10-467-657-5876 Sequence 5876, Ap
45	65.5	7.9	257	6	US-10-467-657-7488 Sequence 7488, Ap

ALIGNMENTS

RESULT 1  
US-10-878-556A-183  
; Sequence 183, Application US/10878556A  
; Publication No. US20050266399A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann La-Roche Inc.  
; TITLE OF INVENTION: HCV regulated protein expression  
; FILE REFERENCE: 21762  
; CURRENT APPLICATION NUMBER: US/10/878,556A  
; CURRENT FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 183  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: sw\_hum/pdx5\_human  
; DATABASE ENTRY DATE: 1993-04-01  
US-10-878-556A-183

Query Match 100.0%; Score 830; DB 6; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.5e-78;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFGKGGVLFPGVPGAFTPGSKTHLPGFVEQA 60  
DB 53 MAPKVGDAIPAVEVEFEGEPGNKVNLAELFGKGGVLFPGVPGAFTPGSKTHLPGFVEQA 112  
QY 61 EALKAGQVAVACISVNDFAFTGEGRAHKAEGKRVRLADPTGAPGKETDLDLSDLSVI 120  
DB 113 EALKAGQVAVACISVNDFAFTGEGRAHKAEGKRVRLADPTGAPGKETDLDLSDLSVI 172  
QY 121 FGNRLKRFPSMVVODGIVKALNVBPDGTGLTCSLAPNIIISQL 162  
DB 173 FGNRLKRFPSMVVODGIVKALNVBPDGTGLTCSLAPNIIISQL 214

RESULT 2  
US-10-467-657-5556  
; Sequence 5556, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta

```
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMin99, version 1.04
/ SEQ ID NO 5556
/ LENGTH: 267
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5556

Query Match          30.4%; Score 252.5; DB 6; Length 267;
Best Local Similarity 38.5%; Pred. No. 8.6e-19;
Matches 57; Conservative 28; Mismatches 56; Indels 7; Gaps 5;

Qy      5 KYGDALPAVEVE---GEPGNKYNLAELFKGKGVLFVGPAGFTPGCSKTHLPGFVEQAE 61
      28 RRGQKPSV-VFRTRGDVMKOVSTDLFKGKVVVFSLPGATPTCSSHLPRVNELRG 86
Db
Qy      62 ALKAGQVAVCLSVNDAFVTGEMGRABKAEKVRLLADPTGAFGKETDLLDDSLVSIF 121
      87 AFKEKGVDAICCVSVNDTFVNNAMA-AEESDNIYIMPDNGEFTEGMGLVGEKEDLG-F 144
Db
Qy      122 GNRRLKFSMVVODGIVKALNVEPDGTG 149
      145 G-KRSWRYSMLVNDGVVERMFIEEPBG 171
Db
```

```
RESULT 3
US-11-058-926-22
/ Sequence 22, Application US/11058926
/ Publication No. US20060030022A1
/ GENERAL INFORMATION:
/ APPLICANT: BECKWITH, JONATHAN
/ APPLICANT: ASLUND, FREDRIK
/ APPLICANT: BESSETTE, PAUL H.
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: RITZ, DANIEL
/ APPLICANT: LIM, JACKIE EUN-AH
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
/ FILE REFERENCE: HMV-052.01
/ CURRENT APPLICATION NUMBER: US/11/058,926
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/679,705
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/157,770
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/163,939
/ PRIOR FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/166,044
/ PRIOR FILING DATE: 1999-11-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 187
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-11-058-926-22
```

```
Query Match          12.9%; Score 107; DB 7; Length 187;
Best Local Similarity 28.6%; Pred. No. 0.00056;
Matches 36; Conservative 22; Mismatches 56; Indels 12; Gaps 5;

Qy      31 KKKGGLFVGPAGFTPGCSKTHLPGFVEQAEALKAGQVAVCLSVNDAFVTGEMGRABK 90
      30 EGRWSVFFFPYADFTVC-PTELGVDADHYEELQKLGVDVYA-VSTDTHTFKAHSSSE 87
Db
Qy      91 AEGKVR--LLADPTGAFGKETDLLDDSLVSIFGNRLKFSMVVQ-DGIVKALNVEPDG 147
      145 G-KRSWRYSMLVNDGVVERMFIEEPBG 171
Db
```

```
Db      88 TIAKIKAMIGDPTGALTRNFDNREDEGLA-----DRATFVVDPGIIQAIETVTAEG 140
Qy      148 TGLTGS 153
Db      141 IGRDAS 146
```

```
RESULT 4
US-11-058-926-24
/ Sequence 24, Application US/11058926
/ Publication No. US20060030022A1
/ GENERAL INFORMATION:
/ APPLICANT: BECKWITH, JONATHAN
/ APPLICANT: ASLUND, FREDRIK
/ APPLICANT: BESSETTE, PAUL H.
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: RITZ, DANIEL
/ APPLICANT: LIM, JACKIE EUN-AH
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
/ FILE REFERENCE: HMV-052.01
/ CURRENT APPLICATION NUMBER: US/11/058,926
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/679,705
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/157,770
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/163,939
/ PRIOR FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/166,044
/ PRIOR FILING DATE: 1999-11-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-11-058-926-24
```

```
Query Match          11.7%; Score 97; DB 7; Length 188;
Best Local Similarity 28.6%; Pred. No. 0.0061;
Matches 34; Conservative 20; Mismatches 53; Indels 12; Gaps 5;

Qy      38 FGVPAFTPGCSKTHLPGFVEQAEALKAGQVAVCLSVNDAFVTGEMGRABKAEKVR- 96
      38 FFPYADFTVC-PTELGVDADHYEELQKLGVDVYA-VSTDTHTFKAHSSSETIAKIX 95
Db
Qy      97 -LLADPTGAFGKETDLLDDSLVSIFGNRLKFSMVVQ-DGIVKALNVEPDGTGLTGS 153
      96 AMIGDPTGALTRNFDNREDEGLA-----DRATFVVDPGIIQAIETVTAEGIGRDAS 147
Db
```

```
RESULT 5
US-10-821-234-1419
/ Sequence 1419, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andamant, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_SEQ Version 1.0
/ SEQ ID NO 1419
/ LENGTH: 271
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```





```
RESULT 13
US-10-485-788A-516
; Sequence 516, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-0032005
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 516
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: post-synaptic desensitly protein 95 (PSD95)
; OTHER INFORMATION: Construct (N-P3) aa 1 - aa 442
US-10-485-788A-516

Query Match          9.5%; Score 78.5; DB 6; Length 442;
Best Local Similarity 27.3%; Pred. No. 1.6;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVPGAFPTGCGSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 197 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 232
Cy 80 FVTG--EMGRANKAEKV---RLADPTGAFGKETDILLDSLVISFGNRLKRFSMNV 133
Db 233 YVTKIIEGGAHK-DGRLOIGDKILA--VNSVGLD-DVMHEDAVAA-----LKNTYDVV 282
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 283 YLKVAK-----PSNAVLSDSYAP 300

RESULT 14
US-11-126-313-28
; Sequence 28, Application US/11126313
; Publication No. US2005028489A1
; GENERAL INFORMATION:
; APPLICANT: Hirsch, Joel
; TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
; FILE REFERENCE: P-6758-US
; CURRENT APPLICATION NUMBER: US/11/126,313
; CURRENT FILING DATE: 2005-05-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-126-313-28

Query Match          9.5%; Score 78.5; DB 7; Length 724;
Best Local Similarity 27.3%; Pred. No. 3;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVPGAFPTGCGSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 197 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 232
```

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Db 154 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 189
Cy 80 FVTG--EMGRANKAEKV---RLADPTGAFGKETDILLDSLVISFGNRLKRFSMNV 133
Db 190 YVTKIIEGGAHK-DGRLOIGDKILA--VNSVGLD-DVMHEDAVAA-----LKNTYDVV 239
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 240 YLKVAK-----PSNAVLSDSYAP 257

RESULT 15
US-11-032-236-4
; Sequence 4, Application US/11032236
; Publication No. US20050273867A1
; GENERAL INFORMATION:
; APPLICANT: BRULET, PHILIPPE
; APPLICANT: ROGERS, KELLY
; APPLICANT: PICAUD, SANDRINE
; TITLE OF INVENTION: NON-INVASIVE REAL-TIME IN VIVO BIOLUMINESCENCE IMAGING
; FILE REFERENCE: 03495-0328
; CURRENT APPLICATION NUMBER: US/11/032,236
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/543,659
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: coding sequence contained in PSDGA vector
US-11-032-236-4

Query Match          9.5%; Score 78.5; DB 7; Length 1219;
Best Local Similarity 27.3%; Pred. No. 6.1;
Matches 39; Conservative 19; Mismatches 40; Indels 45; Gaps 9;

Cy 20 PGNKVNLAELFKGKGGVLFVPGAFPTGCGSKTHLPGFVEQAALAKAGVQVVAACLSVND 79
Db 154 PAKRMEIKLIKPGKGLGFSIAG-----GVGNQHIFG-----DNSI 189
Cy 80 FVTG--EMGRANKAEKV---RLADPTGAFGKETDILLDSLVISFGNRLKRFSMNV 133
Db 190 YVTKIIEGGAHK-DGRLOIGDKILA--VNSVGLD-DVMHEDAVAA-----LKNTYDVV 239
Cy 134 QDGIVKALNVEPDGTGLTCSLAP 156
Db 240 YLKVAK-----PSNAVLSDSYAP 257
```

Search completed: February 21, 2006, 22:01:20  
Job time : 19 secs





1. TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE

```
/ TITLE OF INVENTION: PROTEINS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/959,004
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0414 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 214 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: BRAITUT01
/ CLONE: 743725
/ US-08-959-004-1

Query Match      100.0%; Score 830; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEEGEPGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 60
    |||||
DB 53 MAPIKVGDAIPAVEVEEGEPGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 112
    |||||

QY 61 EALKAGVQVVACTSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSI 120
    |||||
DB 113 EALKAGVQVVACTSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSI 172
    |||||

QY 121 FGNRLKRPMSWVVDGIYKALNVEPDGTLTCSLAPNIISQL 162
    |||||
DB 173 FGNRLKRPMSWVVDGIYKALNVEPDGTLTCSLAPNIISQL 214
    |||||

RESULT 3
US-09-486-167A-4
/ Sequence 4; Application US/09486167A
/ Patent No. 6759194
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
/ TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAI
/ TITLE OF INVENTION: AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG IN
/ FILE REFERENCE: VANM143.001A
/ CURRENT APPLICATION NUMBER: US/09/486,167A
/ CURRENT FILING DATE: 2000-08-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
```

```
/ LENGTH: 162
/ TYPE: PRT
/ ORGANISM: Rattus rattus
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 17
/ OTHER INFORMATION: Glu or Gly
/ NAME/KEY: Modified-site
/ LOCATION: 63
/ OTHER INFORMATION: Leu or Pro
/ NAME/KEY: Modified-site
/ LOCATION: 79
/ OTHER INFORMATION: Ala or Val
/ US-09-486-167A-4

Query Match      90.6%; Score 752; DB 2; Length 162;
Best Local Similarity 88.9%; Pred. No. 5.9e-84;
Matches 144; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEEGEPGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 60
    |||||
DB 1 MAPIKVGDTIPSEVFEKGEPRGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 60
    |||||

QY 61 EALKAGVQVVACTSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSI 120
    |||||
DB 61 GAXKAKGAVVACTSVNDXFTVAEMGRAHQAEGKVQLADPTGAFGKETDLLLDDSLVSI 120
    |||||

QY 121 FGNRLKRPMSWVVDGIYKALNVEPDGTLTCSLAPNIISQL 162
    |||||
DB 121 FGNRLKRPMSWVIDRGVVAALNVEPDGTLTCSLAPNIISQL 162
    |||||

RESULT 4
US-09-513-999C-8124
/ Sequence 8124; Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclet, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59. US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 3681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 8124
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 80
/ OTHER INFORMATION: Xaa=Asp or Glu
/ US-09-513-999C-8124

Query Match      43.9%; Score 364; DB 2; Length 125;
Best Local Similarity 98.6%; Pred. No. 1.5e-36;
Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPIKVGDAIPAVEVEEGEPGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 60
    |||||
DB 53 MAPIKVGDAIPAVEVEEGEPGNKNVLAELFKGKKGVLFVPGAFPTPGCKSTHLPGFVEQA 112
    |||||

QY 61 EALKAGVQVVA 72
    |||||
DB 113 EALKAGVQVVA 124
    |||||

RESULT 5
```

US-09-248-796A-16927  
; Sequence 16927, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NOCLETIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16927  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16927

Query Match 42.8%; Score 355.5; DB 2; Length 202;  
Best Local Similarity 44.1%; Pred. No. 3.3e-35;  
Matches 71; Conservative 25; Mismatches 60; Indels 5; Gaps 2;

QY 4 IKVGDAIPAVEPGEPEGKVNLAELFKGKGVLFVGAFPGCKTHLPQVQEARL 63  
DB 43 VSIGDKVATPVFESPGNDINLAETASGKTIILGVGASPSACSHVGEYKNIAAF 102  
QY 64 KAKGVAVACLVNDAPVYTGEMGR--AKKAGKVRLLADPTGAFGKETDLLDDSLVSI 120  
DB 103 NDKGYQRFVAVNDPFTYKAMGEQLLESVAGQIRFPADSGATTKELDLFDPAR--KA 160  
QY 121 FGNRLKRFMSVVDGIVKALNVEPDGTGLTCSLAPNISQ 161  
DB 161 FGNRSKRKYALIIEDGKVKSFVEBDNITSVDVSAQKVLER 201

RESULT 6  
US-09-513-999C-6299  
; Sequence 6299, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6299  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6299

Query Match 38.0%; Score 315; DB 2; Length 118;  
Best Local Similarity 80.7%; Pred. No. 1.4e-30;  
Matches 67; Conservative 0; Mismatches 6; Indels 10; Gaps 1;

QY 83 GEM-----GRAHRAEGKVRLLADPTGAFGKETDLLDDSLVIFGNRLKRFMSV 132  
DB 36 GEMAGGVRSRRAAAAPIKVRLADPTGAFGKETDLLDDSLVIFGNRLKRFMSV 95  
QY 133 VODGIVKALNVEPDGTGLTCSIA 155  
DB 96 VODGIVKALNVEPDGTGLTCSIA 118

RESULT 7  
US-08-959-004-8

; Sequence 8, Application US/08959004  
; Patent No. 6197543  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/959,004  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0414 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 189 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1652858  
US-08-959-004-8

Query Match 30.4%; Score 252.5; DB 2; Length 189;  
Best Local Similarity 39.8%; Pred. No. 1.3e-22;  
Matches 64; Conservative 27; Mismatches 53; Indels 17; Gaps 7;

QY 8 DAIPAVEYF-----EGBPG-----NKVNLAEFLFKGKGVLFVGPAFTGCKSTHLP 55  
DB 4 ERVPSV-VFKTRVDESGPGPNPYRWEDKTEQIFGKGVLFSLPGAFTGCKSTHLP 62  
QY 56 FVEQAEALKAKGVVAVCLVNDAPVYTGEMGRHAKGKVRLLADPTGAFGKETDLLDD 115  
DB 63 YEQIFEEQALGVDDITCLVNDAPVYFQWCKQIGAD-KVLLPDGNGCFTRKGMVLEK 121  
QY 116 SLVSIFGNRLKRFMSVVDGIVKALNVEPDGTGLTCSLAP 156  
DB 122 SNLG-FGNRSM-RYSMTFVNDGKIKMFIEPE-FDNCPCVDP 159

RESULT 8  
US-09-540-236-2375  
; Sequence 2375, Application US/09540236

/ Patent No. 6673910  
/ GENERAL INFORMATION:  
/ APPLICANT: Gary L. Breton et al.  
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS  
/ FILE REFERENCE: 2709.2005-001  
/ CURRENT APPLICATION NUMBER: US/09/540,236  
/ CURRENT FILING DATE: 2000-04-04  
/ NUMBER OF SEQ ID NOS: 3840  
/ SEQ ID NO 2375  
/ LENGTH: 270  
/ TYPE: PRT  
/ ORGANISM: M. catarrhalis  
US-09-540-236-2375

Query Match 29.1%; Score 241.5; DB 2; Length 270;  
Best Local Similarity 39.0%; Pred. No. 4,7e-21;  
Matches 57; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 7 GAIPAVEVEEGEPGNK--VNLAELFKGKGVLFVGPAPFTPGSKTHLPGVBOEAL 63  
DB 29 GQKVPNA-VFHTROGQWVDVNTDELFSGKVVVPSLPGAFPTGCSSTHLPKYNELADEF 87  
QY 64 KAKGVQVAVCLSVNDAFVTGEMGRAHKAEGVALLADPTGAFGKETDLLLDDSLVSIFGN 123  
DB 88 KKLGIIDILCVSYNDTFVNNAMADQESD-KITLIPDNGEFTGEMNRLVSKEDLG-FG- 144  
QY 124 RLKRSWVVOGIVKALNVEPDGTG 149  
DB 145 KRSWYSMLVDGMIKVIDEPEKDG 170

RESULT 9  
US-08-959-004-7  
/ Sequence 7, Application US/08959004  
/ Patent No. 6197543  
/ GENERAL INFORMATION:  
/ APPLICANT: Hillman, Jennifer L.  
/ APPLICANT: Yue, Henry  
/ APPLICANT: Corley, Neil C.  
/ APPLICANT: Lal, Preeti  
/ APPLICANT: Shah, Purvi  
/ APPLICANT: Kaser, Matthew  
/ TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE  
/ TITLE OF INVENTION: PROTEINS  
/ NUMBER OF SEQUENCES: 11  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.  
/ STREET: 3174 Porter Drive  
/ CITY: Palo Alto  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94304  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSeq for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/959,004  
/ FILING DATE: Herewith  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Billings, Lucy J.  
/ REGISTRATION NUMBER: 36,749  
/ REFERENCE/DOCKET NUMBER: PF-0414 US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 650-855-0555  
/ TELEFAX: 650-845-4166  
/ TELEX:

/ INFORMATION FOR SEQ ID NO: 7:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 167 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ IMMEDIATE SOURCE:  
/ LIBRARY: GenBank  
/ CLONE: 170899  
US-08-959-004-7

Query Match 25.7%; Score 213.5; DB 2; Length 167;  
Best Local Similarity 35.3%; Pred. No. 6,3e-18;  
Matches 60; Conservative 31; Mismatches 68; Indels 11; Gaps 6;

QY 1 MAPIVGAIPIAV-BVF-----EGEPGNKVNLAELFKKKGVLFGVPAPFTPGSKTHLP 54  
DB 1 MAPIRGRFPFTDVIYIPEEGEPG-PLEISKRVKTKRVVSPGAFPTPTGQHLP 59  
QY 55 GPEBOEALKAKGVQVAVCLSVNDAFVTGEMGRAHKAEG-KVRLADPTGAFGKETDLL 112  
DB 60 GYIKLPLILSKGVDFVLVISQNDPFLKGMKEIGAADAKKLVVSPDNLKTLTKLGST 119  
QY 113 LDDSLVSIFGNRLKRFMSVVDGIVKALNVEPDGTGLTCSLAPNIISQL 162  
DB 120 IDLSAIGL-GTFRSGLALIVNRSGLIVEYAAIE-NGGEVDVSTAQKIITAKL 167

RESULT 10  
US-09-091-097-4  
/ Sequence 4, Application US/09091097  
/ Patent No. 6432407  
/ GENERAL INFORMATION:  
/ APPLICANT: TAKESAKO, KAZUTOH  
/ APPLICANT: OKADO, TAKASHI  
/ APPLICANT: YAGIHARA, TOMOKO  
/ APPLICANT: KURODA, MASANOBU  
/ APPLICANT: ONISHI, YOSHIMI  
/ APPLICANT: KATO, IKUNOSHIN  
/ APPLICANT: AKIYAMA, KAZUO  
/ APPLICANT: YASUDA, HIROSHI  
/ APPLICANT: YAMAGUCHI, HIDEYO  
/ TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN  
/ TITLE OF INVENTION: MALASSEZIA  
/ NUMBER OF SEQUENCES: 58  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
/ STREET: PO BOX 747  
/ CITY: FALLS CHURCH  
/ STATE: VA  
/ COUNTRY: USA  
/ ZIP: 22040-0747  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/091,097  
/ FILING DATE:  
/ CLASSIFICATION: 424  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: WEINER, MARC S.  
/ REGISTRATION NUMBER: 32,181  
/ REFERENCE/DOCKET NUMBER: 1422-0346P  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 703-205-8050  
/ TELEFAX: 703-205-8050  
/ INFORMATION FOR SEQ ID NO: 4:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 166 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-091-097-4

Query Match 23.4%; Score 194; DB 2; Length 166;

Best Local Similarity 35.5%; Pred. No. 1.5e-15;

Matches 49; Conservative 21; Mismatches 58; Indels 10; Gaps 3;

QY 28 ELFKGKGVLPFGVPAFTPGCSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTGEMGR 87

DB 36 ERMKQKVVIVAVPAFTPTCTANHVPPYVEKIQELKSKGVDEVVVISANDPVLISAMGI 95

QY 88 AHKAEKVRLLADPTGAFGKETDILLDSLVISIFGNRLKRFSSMVVQDGIKALNV---E 144

DB 96 TEHADNLTFAQDVNCFSPKHNATLD--LSKGMGLRTARYALANDLKVEYFGIDEGE 153

QY 145 PDGTGLTSLAPNIISOL 162

DB 154 PKQ-----SSAATVLSKL 166

RESULT 11

US-10-109-670-9

Sequence 9, Application US/10109670

Patent No. 6911208

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH et al.

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA

FILE REFERENCE: 1422-0523P

CURRENT APPLICATION NUMBER: US/10/109,670

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 9

LENGTH: 166

TYPE: PRT

ORGANISM: Malassezia furfur

US-10-109-670-9

Query Match 23.4%; Score 194; DB 2; Length 166;

Best Local Similarity 35.5%; Pred. No. 1.5e-15;

Matches 49; Conservative 21; Mismatches 58; Indels 10; Gaps 3;

QY 28 ELFKGKGVLPFGVPAFTPGCSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTGEMGR 87

DB 36 ERMKQKVVIVAVPAFTPTCTANHVPPYVEKIQELKSKGVDEVVVISANDPVLISAMGI 95

QY 88 AHKAEKVRLLADPTGAFGKETDILLDSLVISIFGNRLKRFSSMVVQDGIKALNV---E 144

DB 96 TEHADNLTFAQDVNCFSPKHNATLD--LSKGMGLRTARYALANDLKVEYFGIDEGE 153

QY 145 PDGTGLTSLAPNIISOL 162

DB 154 PKQ-----SSAATVLSKL 166

RESULT 12

US-09-091-097-2

Sequence 2, Application US/09091097

Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH

APPLICANT: OKADO, TAKASHI

APPLICANT: YAGIHARA, TOMOKO

APPLICANT: KURODA, MASANOBU

APPLICANT: ONISHI, YOSHIMI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: AKIYAMA, KAZUO

APPLICANT: YASUEDA, HIROSHI

APPLICANT: YAMAGUCHI, HIDEYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: PO BOX 747  
CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,097

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 176 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-091-097-2

Query Match 23.0%; Score 191; DB 2; Length 176;

Best Local Similarity 35.8%; Pred. No. 3.9e-15;

Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY 30 FKGGKGVLPFGVPAFTPGCSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTGEMGR 89

DB 45 WKGRKVVIVSIPGAYTPICHQOHLPVVKRVDLAKAGVAVVYIASNDPVMAMAGNFN 104

QY 90 KAEKVRLLADPTGAFGKETDILLDSLVISIFGNRLKRFSSMVVQDGIKALNVPEPDGTG 149

DB 105 NAKQKVPADIDIALFSAKALGATIDLS-AKHFG-ERTARYALIIDDKYIDFASDEGDTG 162

RESULT 13

US-10-109-670-8

Sequence 8, Application US/10109670

Patent No. 6911208

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH et al.

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA

FILE REFERENCE: 1422-0523P

CURRENT APPLICATION NUMBER: US/10/109,670

CURRENT FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 8

LENGTH: 176

TYPE: PRT

ORGANISM: Malassezia furfur

US-10-109-670-8

Query Match 23.0%; Score 191; DB 2; Length 176;

Best Local Similarity 35.8%; Pred. No. 3.9e-15;

Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY 30 FKGGKGVLPFGVPAFTPGCSKTHLPGFVEQAEALAKAGVQVAVCLSVNDAFVTGEMGR 89

DB 45 WKGRKVVIVSIPGAYTPICHQOHLPVVKRVDLAKAGVAVVYIASNDPVMAMAGNFN 104

QY 90 KAEKVRLLADPTGAFGKETDILLDSLVISIFGNRLKRFSSMVVQDGIKALNVPEPDGTG 149

DB 105 NAKQKVPADIDIALFSAKALGATIDLS-AKHFG-ERTARYALIIDDKYIDFASDEGDTG 162

RESULT 14

```
US-09-091-097-19
; Sequence 19, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIMI
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-091-097-19

Query Match      23.0%; Score 191; DB 2; Length 177;
Best Local Similarity 35.8%; Pred. No. 3.9e-15;
Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY      30 FRGKKGVLFVGPAFTPGCSKTHLPGFVBOALAKAGVAVACLSVNDAPFTGEMGRAH 89
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      46 WKGKKVVISIPGATTPICHQCHIPPLVKRVDELAKAGVDAYVYIASNDPFVMAAMGNFN 105
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      90 KAEGKVRLLADPTGAFGKETDILLDDSLVSIFGNRLKRFMSWVODGIKALNVEPDGTG 149
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      106 NAKDKRVFATDIDLAFSKALGATIDLS-AKHFG-ERTARVALLIDNKKIVDFASDEGDTG 163
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-10-109-670-19
; Sequence 19, Application US/10109670
; Patent No. 6911208
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 19
; LENGTH: 177
```

```
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-19

Query Match      23.0%; Score 191; DB 2; Length 177;
Best Local Similarity 35.8%; Pred. No. 3.9e-15;
Matches 43; Conservative 21; Mismatches 54; Indels 2; Gaps 2;

QY      30 FRGKKGVLFVGPAFTPGCSKTHLPGFVBOALAKAGVAVACLSVNDAPFTGEMGRAH 89
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      46 WKGKKVVISIPGATTPICHQCHIPPLVKRVDELAKAGVDAYVYIASNDPFVMAAMGNFN 105
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      90 KAEGKVRLLADPTGAFGKETDILLDDSLVSIFGNRLKRFMSWVODGIKALNVEPDGTG 149
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      106 NAKDKRVFATDIDLAFSKALGATIDLS-AKHFG-ERTARVALLIDNKKIVDFASDEGDTG 163
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: February 21, 2006, 21:47:47
Job time : 48 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:38:52 ; Search time 186 Seconds  
(without alignments)  
382.685 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKGVDAIPAVEVFEEGP.....VEPDGTGLTCSLAPNIIISQL 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	162	2	AAV01079 Human bro
2	830	100.0	162	2	AdJ70346 Human hea
3	830	100.0	205	4	ABE11403 Human Ali
4	830	100.0	214	2	AAV17388 Human ves
5	830	100.0	214	7	AdJ68964 Human hea
6	830	100.0	214	7	ADM83091 Human ves
7	830	100.0	214	9	ADM08846 Human pro
8	830	100.0	214	9	AdY81123 Human bra
9	830	100.0	214	9	AEa17061 Alzheim
10	825	99.4	161	7	AdJ70591 Human hea
11	818	98.6	214	4	AAJ78658 Human per
12	777	93.6	226	5	ABP42382 Human ova
13	701	84.5	194	6	ABU00319 Human nov
14	667	80.4	150	4	AAE87638 Bovine ma
15	573	65.0	169	7	AdC14210 Human enz
16	569	68.6	351	4	ABG20681 Novel hum
17	568	68.4	170	6	ABU00321 Human nov
18	498	60.0	137	4	ADG27703 Human nov
19	479	57.7	157	4	ABH63096 Drosophil
20	469.5	56.6	285	4	ABG09401 Novel hum
21	364	43.9	125	3	AAJ04043 Human sec
22	346	41.7	130	5	ABP42342 Human ova
23	315	36.0	118	3	AAJ02218 Human sec
24	310	37.3	162	8	ADM48269 Polypepti

25	310	37.3	248	8	ADX88783 Plant ful
26	294	35.4	162	3	AAJ05212 Arabidops
27	294	35.4	179	3	AAJ05211 Arabidops
28	289.5	34.9	234	8	ADT56507 Plant pol
29	289	34.8	162	3	AAJ10272 Arabidops
30	288	34.7	162	3	AAJ38202 Arabidops
31	288	34.7	162	7	ADL18519 Rice thio
32	288	34.7	162	7	ADJ11372 Rice prot
33	288	34.7	162	7	ADJ11814 Rice prot
34	288	34.7	162	7	ABM90086 Rice abio
35	288	34.7	179	3	AAJ38201 Arabidops
36	286	34.5	162	3	AAJ38958 Arabidops
37	286	34.5	162	3	AAJ11980 Arabidops
38	286	34.5	162	6	ABP81187 Arabidops
39	286	34.5	182	3	ADP81187 Arabidops
40	280	33.7	162	7	ADL18521 Arabidops
41	277	33.4	162	3	AAJ10252 Arabidops
42	277	33.4	180	3	AAJ10251 Arabidops
43	263	31.7	164	7	ABM89372 Rice abio
44	259.5	31.3	126	3	AAJ38450 Arabidops
45	255	30.7	160	7	ABM90200 Rice abio

#### ALIGNMENTS

RESULT 1	AAV01079	standard; protein, 162 AA.
ID	AAV01079	
AC	AAV01079;	
DT	08-JUN-1999	(first entry)
DE	Human bronchoalveolar polypeptide, B18hum.	
XX	B18hum; bronchoalveolar protein; peroxisome-associated polypeptide;	
XX	lung injury; oxidative stress-related disorder; inflammatory disease;	
XX	cardiovascular disease; neurodegenerative disorder; allergic reaction;	
XX	amyotrophic lateral sclerosis; apoptosis; high bone mass syndrome;	
XX	osteopetrosis; osteoporosis-pseudoglioma syndrome; diagnosis;	
XX	Bardet-Biedl syndrome 1; therapy4.	
OS	Homo sapiens.	
XX	FN	WO9909054-A2;
XX	PD	25-FEB-1999.
XX	PF	20-AUG-1998; 98WO-BE000124.
XX	PR	20-AUG-1997; 97BE-00000692.
XX	PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX	PA	(UWMO-) UNIV MONS-HAINAUT.
XX	PI	Knoops B, Hermans C, Bernard A, Mattiez R, Falmagne P;
XX	DR	WPI; 1999-180968/15.
XX	DR	N-PSDB; AAX27965.
XX	PT	New low molecular weight human broncho-alveolar polypeptide - useful for
XX	PT	diagnosis and/or treatment of lung injuries and diseases, and oxidative
XX	PS	stress-related diseases and disorders, especially inflammatory diseases.
XX	PS	Claim 4; Page 33-34; 45pp; English.
CC	This sequence is the human bronchoalveolar polypeptide, designated B18hum	
CC	of the invention. B18hum is a low molecular weight human, peroxisome-	
CC	associated broncho-alveolar polypeptide. A diagnostic device featuring	
CC	the polypeptide, polynucleotide and/or inhibitor is useful for in vitro	
CC	detection of lung injuries and diseases or oxidative stress-related	
CC	diseases and disorders, especially inflammatory diseases. The device is	

CC also useful for monitoring such diseases or disorders in patients or  
 CC fluid samples. The polypeptide, polynucleotide and inhibitor form  
 CC pharmaceutical compositions useful in the prevention and/or treatment of  
 CC these diseases or disorders, especially specific cardio-vascular diseases  
 CC (e.g. atherosclerosis), neurodegenerative disorders (e.g. Alzheimer's  
 CC disease and Parkinson's disease), amyotrophic lateral sclerosis,  
 CC apoptosis and inflammatory reactions, allergic reactions (e.g. asthma,  
 CC hay fever and eczema), high bone mass syndrome, osteoporosis,  
 CC osteoporosis-pseudoglioma syndrome, and Bardet-Biedl syndrome 1. The  
 CC polypeptide is also useful as a specific marker of the above diseases or  
 CC disorders in a wide variety of tissues. The discovery of the peroxisome-  
 CC associated polypeptide enables the development of diagnosis and treatment  
 CC of peroxisomal disorders

XX Sequence 162 AA:

Query Match 100.0%; Score 830; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-90;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEEBSGKKNVLAELFKGKGVLPQVPAFPGSKTHLPQVQA 60  
 Db 1 MAPIKVGDALPAVEVEEBSGKKNVLAELFKGKGVLPQVPAFPGSKTHLPQVQA 60  
 QY 61 EALKAKGVVAVCLSVNDAFVTGEMGRAHKAEGKRVRLADPTGAFGKETDLLDDSLVSI 120  
 Db 61 EALKAKGVVAVCLSVNDAFVTGEMGRAHKAEGKRVRLADPTGAFGKETDLLDDSLVSI 120

QY 121 FGNRLKRPSSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 Db 121 FGNRLKRPSSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162

RESULT 2

ADJ70346 standard; protein; 162 AA.

ADJ70346;

06-MAY-2004 (first entry)

Human heat mitochondrial protein as a therapeutic target SeqID2152.

mitochondrial; human; screening assay; diabetes mellitus;

Huntington's disease; osteoarthritis;

Leber's hereditary optic neuropathy; LHON;

mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

osteopathic; ophthalmological; cyostatic.

Homo sapiens.

WO2003087768-A2.

23-OCT-2003.

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P.

17-JUN-2002; 2002US-0389887P.

20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR.

(BUCK-) BUCK INST AGE RES.

Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

Warnock DE;

WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for  
 treating diseases associated with altered mitochondrial function.

PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.

PS Claim 1; SEQ ID NO 2152; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nootropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cyostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX Sequence 162 AA:

Query Match 100.0%; Score 830; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-90;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEEBSGKKNVLAELFKGKGVLPQVPAFPGSKTHLPQVQA 60  
 Db 1 MAPIKVGDALPAVEVEEBSGKKNVLAELFKGKGVLPQVPAFPGSKTHLPQVQA 60  
 QY 61 EALKAKGVVAVCLSVNDAFVTGEMGRAHKAEGKRVRLADPTGAFGKETDLLDDSLVSI 120  
 Db 61 EALKAKGVVAVCLSVNDAFVTGEMGRAHKAEGKRVRLADPTGAFGKETDLLDDSLVSI 120

QY 121 FGNRLKRPSSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 Db 121 FGNRLKRPSSMVVQDGIYKALNVEPDGTGLTCSLAPNIISQL 162

RESULT 3

ABBI1403 standard; peptide; 205 AA.

ABBI1403;

11-JAN-2002 (first entry)

Human Alu co-repressor I homologue, SEQ ID NO:1773.

Human; cytokine; cell proliferation; cell differentiation; growth factor;

haematopoiesis regulation; tissue growth; immunomodulator; activin;

inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;

proliferation; metastasis; cancer; tumour; haematopoietic disorder;

myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

chronic inflammatory condition; proliferative retinopathy;

atherosclerosis; coronary heart disease; arterial ischaemia;

bone disorder; osteoporosis; vascular growth disorder;

tissue regeneration; wound healing; infection; immune disorder;

cell culture; drug screening; gene therapy; antiinflammatory;

antiallergic; antiarthritic; haemostatic; antiatherosclerotic;

KW cyostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

antifungal; vulneryary; antitumor.

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US003800.

03-FEB-2000; 2000US-00496914.



PR 27-APR-2000; 2000US-00560875.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-457740/49.  
 DR N-PSDB; ABA06647.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing, treating  
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.  
 XX  
 PS Claim 20; Page 179; 1963pp; English.  
 XX  
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention  
 CC  
 XX  
 SQ Sequence 205 AA;  
 Query Match 100.0%; Score 830; DB 4; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-90;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAV17388  
 ID AAV17388 standard; protein; 214 AA.  
 XX  
 AC AAV17388;  
 XX  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE Human vesicle membrane protein-like protein 1.  
 XX  
 KW Human, vesicle membrane protein-like protein; VMP; Cushing's syndrome;  
 KW developmental disorder; vesicle-trafficking disorder; cystic fibrosis;  
 KW immunological disorder; reproductive disorder; neoplastic disorder;  
 KW anaemia; muscular dystrophy; cataract; Grave's disease; allergy;  
 KW ulcerative colitis; microbial infection; Addison's disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M09921994-A2.  
 XX  
 PD 06-MAY-1999.  
 XX  
 PF 14-OCT-1998; 98MO-US021730.  
 XX  
 PR 28-OCT-1997; 97US-00959004.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Hillman UL, Yue H, Corley NC, Lal P, Shah P;  
 XX  
 DR WPI; 1999-326702/27.  
 XX  
 DR N-PSDB; AAX56411.  
 XX  
 PT Human vesicle membrane-like proteins, useful for diagnosis, treatment and  
 PT prevention of e.g. developmental disorders.  
 XX  
 PS Claim 1; Fig 1; 105pp; English.  
 XX  
 CC The present sequence represents human vesicle membrane protein-like  
 CC protein 1 (VMP-1). VMP proteins, and their fragments, are used to treat  
 CC or prevent developmental or vesicle-trafficking disorders, while their  
 CC antagonists are used to treat or prevent immunological, reproductive or  
 CC neoplastic disorders. Typical of many such disorders are anaemia;  
 CC Cushing's syndrome; muscular dystrophy; cataract; cystic fibrosis;  
 CC Grave's disease; ulcerative colitis; allergies; microbial infections;  
 CC Addison's disease; cancer of breast, testis and prostate. VMP proteins  
 CC are also used to raise specific antibodies (used to detect VMP in  
 CC immunoassays (for diagnosis or monitoring), in competitive drug screens  
 CC and to purify VMP from natural sources) and to screen for specific  
 CC antagonists (potential therapeutic agents). VMP polynucleotides or their  
 CC fragments, are used in hybridization assays to detect VMP in biological  
 CC samples (e.g. for diagnosis, including detection of mutations and  
 CC polymorphisms), optionally after amplification, to express recombinant  
 CC VMP, including in vivo for gene therapy, and to map the corresponding  
 CC genomic sequence  
 CC  
 XX  
 SQ Sequence 214 AA;  
 Query Match 100.0%; Score 830; DB 2; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Seq Sequence 214 AA;  
Query Match 100.0%; Score 830; DB 7; Length 214;  
Best Local Similarity 100.0%; Pred. No. 7.3e-90;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 60  
Db 53 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 112  
Qy 61 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
Db 113 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172  
Qy 121 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISOL 162  
Db 173 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISOL 214  
RESULT 7  
ADM08846  
ID ADM08846 standard; protein; 214 AA.  
AC ADM08846;  
XX  
XX  
XX 24-MAR-2005 (first entry)  
DT  
XX  
XX Human protein which is up-regulated in HCV-infected tissue - SEQ ID 183.  
DE  
XX gene targeting; hepatitis C virus infection; protein deactivation;  
KW  
XX protein activation.  
XX  
XX Homo sapiens.  
OS  
XX EP1493750-A2.  
PN  
XX 05-JAN-2005.  
PD  
XX 28-JUN-2004; 2004EP-00015098.  
PE  
XX 30-JUN-2003; 2003GB-00015248.  
PR  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA  
XX Berndt P, Kilby PM, Rugman P;  
PI  
XX WPI; 2005-050476/06.  
DR  
XX  
XX New targets for an antiviral compound having at least one down- and up-  
PT regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
PT outcomes, treating or preventing HCV infections.  
PS  
XX Claim 1; SEQ ID NO 183; 346bp; English.  
CC The invention comprises the amino acid sequences of protein targets for  
CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
CC invention are either up-regulated or down-regulated in HCV-infected  
CC tissue. The proteins of the invention are useful in the preparation of a  
CC medicament for the treatment or prevention of HCV infection. The present  
CC amino acid sequence represents a human protein of the invention which is  
CC up-regulated in HCV-infected tissue.  
XX  
XX  
XX Sequence 214 AA;  
Query Match 100.0%; Score 830; DB 9; Length 214;  
Best Local Similarity 100.0%; Pred. No. 7.3e-90;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 60  
Db 53 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 112  
Qy 61 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120

Db 113 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172  
Qy 121 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISOL 162  
Db 173 FGNRLKRFMSVWVDGIVKALNVEPDGTGLTCSLAPNIISOL 214  
RESULT 8  
ADY81123  
ID ADY81123 standard; protein; 214 AA.  
AC ADY81123;  
XX  
XX  
XX 16-JUN-2005 (first entry)  
DT  
XX  
XX Human brain damage-related disorder marker, peroxiredoxin.  
DE  
XX diagnosis; neurological disease; neuroprotective; nootropic;  
KW Alzheimer's disease; Pick's disease; Parkinson's disease; degeneration;  
KW cerebroprotective; antiparkinsonian; peroxiredoxin.  
XX  
XX Homo sapiens.  
OS  
XX WO2005029088-A2.  
PN  
XX 31-MAR-2005.  
PD  
XX 20-SEP-2004; 2004WO-GB050012.  
PE  
XX 20-SEP-2003; 2003GB-00022063.  
PR 23-JUN-2004; 2004GB-00014089.  
PR 27-AUG-2004; 2004GB-00019068.  
XX  
XX (UYGE-) UNIV GENEVE.  
PA (LUCAS/) LUCAS B.  
PI  
XX Hochstrasser DF, Sanchez J, Leaucuyer P, Allard L;  
PI WPI; 2005-242643/25.  
DR  
XX  
XX Diagnosing a brain damage-related disorder or its possibility in a  
PT subject suspected of suffering from it comprises detecting at least one  
PT polypeptide such as A-FABP or its variant or mutant in a sample of body  
PT fluid.  
PS  
XX Disclosure; SEQ ID NO 15; 92bp; English.  
CC  
XX The invention relates to a method of diagnosing a brain damage-related  
CC disorder or its possibility in a subject suspected of suffering from it.  
CC The method is useful for diagnostic, prognostic and therapeutic  
CC applications relating to brain damage-related disorders. The method is  
CC useful for diagnosing a brain damage-related disorder such as  
CC cerebrovascular, dementia and neurodegenerative diseases, head trauma,  
CC ischemic stroke, hemorrhagic stroke, subarachnoid hemorrhage, intra  
CC cranial hemorrhage, transient ischemic attack, vascular dementia,  
CC Alzheimer's disease, Pick's disease, Parkinson's syndromes, CJD and other  
CC related disorders. The present sequence represents the amino acid  
CC sequence of a human brain damage-related disorder marker, peroxiredoxin.  
XX  
XX  
XX Sequence 214 AA;  
Query Match 100.0%; Score 830; DB 9; Length 214;  
Best Local Similarity 100.0%; Pred. No. 7.3e-90;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 60  
Db 53 MAPIKVGDAIPAVEVEFEGEPGNKYNLAELFKGKKGVLFVGPAGFTPGCSKTHLPGFVBOA 112  
Qy 61 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
Db 113 EALKAKGVQVAVACLSVNDAFVTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 172

OY 121 FGNRLKRFSMVVDGIYKALNVEPDGTGLTCSLAPNIISQL 162  
 DB 173 FGNRLKRFSMVVDGIYKALNVEPDGTGLTCSLAPNIISQL 214

RESULT 9  
 ID AEA17061 standard; protein; 214 AA.

AEAI7061;

11-AUG-2005 (first entry)

Alzheimer's disease associated protein #10.

neuroprotective; nootropic; gene therapy; neurodegenerative disorder;  
 Alzheimer's disease; detection.

Homo sapiens.

US2005123962-A1.

09-JUN-2005.

26-OCT-2004; 2004US-00974148.

28-OCT-2003; 2003US-0515536P.

(AGYT-) AGY THERAPEUTICS INC.

Gan L, Gonzalez-Zulueta M, Ye S, Uffer R, Nikolich K;

WPI: 2005-416976/42.

N-PSDB; AEA17060.

DR Detecting a (susceptibility to a) neurodegenerative disorder in a  
 PT subject, comprises detecting differential expression of an Alzheimer's  
 PT disease associated gene in a biological sample from the subject.

PS Claim 1; SEQ ID NO 20; 131pp; English.

XX The invention relates to a method of detecting neurodegenerative disorder  
 CC or susceptibility to such a disorder in a subject in a sample from the  
 CC subject differential expression of a gene encoding a polypeptide  
 CC comprising a linear sequence of at least 8 amino acids, which is  
 CC essentially identical to a contiguous fragment of 8 amino acids found in  
 CC any of SEQ ID Nos 2-54 (even SEQ ID No8). (M1) is useful for detecting a  
 CC neurodegenerative disorder or susceptibility to a neurodegenerative  
 CC disorder in a subject. The neurodegenerative disorder is characterized by  
 CC a property chosen from neuronal loss, amyloid abgr; plaque formation,  
 CC mononuclear phagocyte activation and mononuclear phagocyte neurotoxicity,  
 CC where the neurodegenerative disorder is Alzheimer's disease. This  
 CC sequence corresponds to a differentially expressed protein detected by  
 CC the method of the invention.

XX Sequence 214 AA;

Query Match 100.0%; Score 830; DB 9; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-90;  
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAPIKYGDALPAVEVEGEPGNKVNLAELFKGKGVLPFGPGAFTPGCSKTHLPGFVEOA 60

DB 53 MAPIKYGDALPAVEVEGEPGNKVNLAELFKGKGVLPFGPGAFTPGCSKTHLPGFVEOA 112

OY 61 EALKAGVQVAVLSTVNDAPVTGEMGRANKAEKGVLLADPTGAFKERTDLLDDSLVSI 120

DB 113 EALKAGVQVAVLSTVNDAPVTGEMGRANKAEKGVLLADPTGAFKERTDLLDDSLVSI 172

OY 121 FGNRLKRFSMVVDGIYKALNVEPDGTGLTCSLAPNIISQL 162

DB 173 FGNRLKRFSMVVDGIYKALNVEPDGTGLTCSLAPNIISQL 214

RESULT 10

ID ADJ70591 standard; protein; 161 AA.

ADJ70591;

06-MAY-2004 (first entry)

Human heat mitochondrial protein as a therapeutic target SeqID2397.

mitochondrial; human; screening assay; diabetes mellitus;

Huntington's disease; osteoarthritis;

Leber's hereditary optic neuropathy; LHON;

mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

osteopathic; ophthalmological; cyostatic.

Homo sapiens.

WO2003087768-A2.

23-OCT-2003.

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P.

17-JUN-2002; 2002US-038987P.

20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR.

(BUCK-) BUCK INST AGE RES.

Ghosh SE, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

Warrock DE;

WPI: 2003-845369/78.

DR Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

PS Claim 1; SEQ ID NO 2397; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nootropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cyostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX Sequence 161 AA;

Query Match 99.4%; Score 825; DB 7; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-89;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 APIKYGDALPAVEVEGEPGNKVNLAELFKGKGVLPFGPGAFTPGCSKTHLPGFVEOA 61

DB 1 APIKYGDALPAVEVEGEPGNKVNLAELFKGKGVLPFGPGAFTPGCSKTHLPGFVEOA 60



Query Match 93.6%; Score 777; DB 5; Length 226;  
 Best Local Similarity 95.1%; Pred. No. 1.6e-83;  
 Matches 154; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60  
 |||  
 DB 52 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 111  
 |||

QY 61 EALKKAGVQVVAACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
 |||  
 DB 112 EALKKAGVQVVAACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 171  
 |||

QY 121 FGNRLKRFPSMVVQDGIIVKALNVEPDGTGLTCSLAPNIISQL 162  
 |||  
 DB 172 FGNRLKRFPSMVVQDGIIVKALNVEPDGTGLTCSLAPNIISQL 213  
 |||

RESULT 13  
 ABU00319  
 ID ABU00319 standard; protein; 194 AA.  
 XX  
 AC ABU00319;  
 XX  
 DT 17-JAN-2003 (first entry)  
 XX  
 DE Human novel polypeptide #412.  
 XX  
 KW Human; genetic disorder; gene mapping; medical imaging; cancer;  
 neurodegenerative disorder; lymphoid cell disorder; osteoporosis;  
 Parkinson's disease; Alzheimer's disease; bone degenerative disorder;  
 osteoarthritis; periodontal disease; liver fibrosis; viral infection;  
 fungal infection; bacterial infection; autoimmune disease; diabetes;  
 atopic dermatitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200274961-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 14-MAR-2002; 2002WO-US005109.  
 XX  
 PR 15-MAR-2001; 2001US-00810173.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehtman T, Wang J, Wang D, Drmanac RT;  
 XX  
 DR WPI; 2003-040556/03.  
 XX  
 PT N-PSDB; ABX05397.  
 XX  
 PT New isolated polypeptides and polynucleotides, useful for preventing,  
 treating or ameliorating medical conditions, such as cancer,  
 neurodegenerative disorders, lymphoid cell disorders, bone degenerative  
 disorders, and infections.  
 XX  
 PS Claim 9; SEQ ID NO 938; 235pp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 encode. The polynucleotides and polypeptides are useful in diagnostics,  
 forensics, gene mapping, medical imaging, identification of mutations,  
 responsible for genetic disorders or other traits, assessing biodiversity  
 and producing many other types of data and products dependent on DNA and  
 amino acid sequences. They are also useful for preventing, treating or  
 ameliorating medical conditions, such as cancer, neurodegenerative  
 disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell  
 disorders, osteoporosis, osteoarthritis, bone degenerative disorders,  
 periodontal disease, liver fibrosis, infections (e.g. viral, fungal or  
 bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).  
 CC Sequences ABG9888-ABG9989 and ABU0010-ABU00433 represent human  
 CC polypeptides of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence  
 CC information supplied by the European Patent Office  
 XX  
 SQ Sequence 194 AA;

Query Match 84.5%; Score 701; DB 6; Length 194;  
 Best Local Similarity 87.7%; Pred. No. 1.5e-74;  
 Matches 142; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60  
 |||  
 DB 53 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 112  
 |||

QY 61 EALKKAGVQVVAACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 120  
 |||  
 DB 113 EALKKAGVQVVAACLSVNDAPFTGEMGRAHKAEGKVRLLADPTGAFGKETDILLDDSLVSI 152  
 |||

QY 121 FGNRLKRFPSMVVQDGIIVKALNVEPDGTGLTCSLAPNIISQL 162  
 |||  
 DB 153 FGNRLKRFPSMVVQDGIIVKALNVEPDGTGLTCSLAPNIISQL 194  
 |||

RESULT 14  
 AAB87638  
 ID AAB87638 standard; protein; 150 AA.  
 XX  
 AC AAB87638;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Bovine mammary tissue derived protein #29.  
 XX  
 KW Bovine; mammary gland; cancer; tumour; angiogenesis.  
 XX  
 OS Bos taurus.  
 XX  
 PN WO200114553-A1.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 23-AUG-2000; 2000WO-NZ000166.  
 XX  
 PR 23-AUG-1999; 99US-0150330P.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
 XX  
 PI Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;  
 XX  
 DR WPI; 2001-226619/23.  
 XX  
 PT New polypeptides and polynucleotides encoding the polypeptides, which are  
 expressed in bovine mammary gland tissue, useful for stimulating mammary  
 PT gland growth or function, or inducing differentiation of milk producing  
 PT cells.  
 XX  
 PS Claim 11; Page 72; 97pp; English.  
 XX  
 CC The present invention relates to proteins derived from bovine mammary  
 CC gland cells. The invention is useful for stimulating bovine mammary gland  
 CC cell growth and function, inhibiting the growth of various mammary gland  
 CC cancer cells, inhibiting angiogenesis and vascularization of tumours, or  
 CC modulating the growth of blood vessels in a mammal  
 XX  
 SQ Sequence 150 AA;

Query Match 80.4%; Score 667; DB 4; Length 150;  
 Best Local Similarity 87.0%; Pred. No. 1.1e-70;  
 Matches 127; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 60  
 |||  
 DB 5 MAPIKVGDALPAVEVEFGEPGKKNVLAELFKGKGVLFVGPAGFTPGGSKTHLPGFVEQA 64  
 |||

```

CC polypeptides and polymucleotides are useful in diagnosing, treating and
CC preventing diseases or conditions associated with the decreased
CC expression or overexpression of ENZM, such as cell proliferative (e.g.
CC cancer, atherosclerosis), endocrine (e.g. diabetes), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies), developmental (e.g. Hypochyroidism, Cushing's syndrome),
CC reproductive and vesicle-trafficking disorders, or infections. These are
CC also useful in assessing the effects of exogenous compounds on the
CC expression of nucleic acid and amino acid sequences of ENZM. The ENZM or
CC its fragments are useful in screening compounds for effectiveness as
CC agonist or antagonist of the polypeptides, or in altering the expression
CC of the target polymucleotide and compounds that specifically bind to or
CC modulate the activity of the polypeptide. The microarray is useful in
CC monitoring or measuring protein-protein interactions, drug-target
CC interactions, and gene expression profiles. The sequences shown in
CC ADCl4195-ADCl4247 represent ENZM proteins of the invention.
CX
SQ Sequence 169 AA;
Query Match          69.0%; Score 573; DB 7; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      50 KTHLPGFVEQAELKAKGVVAVCLSVNDAFVTGEMGRABHKAEGKYRLIADPTGAFGKET    109
       |||||
DB      57 KTHLPGFVEQAELKAKGVVAVCLSVNDAFVTGEMGRABHKAEGKYRLIADPTGAFGKET    116
QY      110 DLLDDSLVSI FGNRRRLKRFSMVVQDGI VKALNVDPDGTGLTCSLAPNIISQL    162
       |||||
DB      117 DLLDDSLVSI FGNRRRLKRFSMVVQDGI VKALNVDPDGTGLTCSLAPNIISQL    169

Search completed: February 21, 2006, 21:42:15
Job time : 190 secs

```





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:42:32 ; Search time 39 Seconds  
(without alignments)  
399.670 Million cell updates/sec

Title: US-10-686-157-2

Perfect score: 830

Sequence: 1 MAPIKVGDALPAVEFEGEP.....VEPDGTGLTCSLAPNIISQL 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630.5	76.0	209	2	peroxiredoxin V -
2	317	38.2	191	2	thiol peroxidase (
3	312.5	37.7	160	2	AhpC/ISA family pr
4	303	36.5	161	2	hypothetical prote
5	303	36.5	161	2	peroxiredoxin (imp
6	297.5	35.8	157	2	probable antioxidant
7	294	35.4	162	2	peroxiredoxin-like
8	289.5	34.9	234	2	peroxiredoxin-1 like
9	286	34.5	162	2	peroxiredoxin-like
10	275.5	33.2	251	2	peroxiredoxin 2 fa
11	252.5	30.4	189	2	membrane protein -
12	250.5	30.2	245	2	peroxiredoxin 2 fa
13	243.5	29.3	247	2	peroxiredoxin fami
14	225.5	27.2	243	2	probable peroxidat
15	219.5	26.4	241	2	conserved hypothet
16	219	26.4	178	2	hypothetical 21.4k
17	219	26.4	178	2	peroxisomal membra
18	216	26.0	156	2	peroxisomal membra
19	213.5	25.7	167	2	hypothetical prote
20	210	25.3	553	2	conserved hypothet
21	209.5	25.2	179	2	peroxisomal membra
22	208.5	25.1	167	2	hypothetical prote
23	194	23.4	164	2	allergen Mal f3 -
24	191.5	23.1	166	2	allergen Mal f2 -
25	191	23.0	177	2	probable antioxidant
26	147	17.7	176	2	alanyl hydroperoxid
27	115	13.9	195	2	B15C protein - bar
28	114.5	13.8	215	2	
29	114	13.7	218	2	

30	109	13.1	187	2	alanyl hydroperoxid
31	108	13.0	211	2	alanyl hydroperoxid
32	107.5	13.0	215	2	hypothetical prote
33	107.5	13.0	222	2	alanyl hydroperoxid
34	107	12.9	168	2	hypothetical prote
35	107	12.9	187	2	alanyl hydroperoxid
36	107	12.9	187	2	alanyl hydroperoxid
37	107	12.9	187	2	alanyl hydroperoxid
38	104.5	12.6	207	2	antioxidant, AhpC/
39	104	12.5	187	2	antioxidant, AhpC/
40	102.5	12.3	153	2	bacterioferritin c
41	102.5	12.3	157	2	bacterioferritin c
42	101.5	12.2	220	2	RAB24 protein - ri
43	101	12.2	216	2	probable peroxidat
44	101	12.2	216	2	probable alanyl hyd
45	98.5	11.9	250	2	probable thioredox

## ALIGNMENTS

## RESULT 1

UCJ7239

peroxiredoxin V - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C:Accession: J07239

R:Lee, T.H.; Kim, S.J.; Kang, S.W.; Lee, K.K.; Rhee, S.G.; Yu, D.Y.

Biochem. Biophys. Res. Commun. 270, 356-362, 2000

A:Title: Molecular cloning and characterization of the mouse peroxiredoxin V gene.

A:Reference number: J07239

A:Accession: J07239

A:Molecule type: mRNA

A:Residues: 1-209 <LRR>

A:Cross-references: UNIPROT:P99029; UNIPARC:UPI000016C928; GB:AF208729

A:Experimental source: liver

A:Comment: This protein, thiol-specific antioxidant, belonging to peroxiredoxin family, oxidizes, and influences the differentiation, proliferation, activity and survival of

C:Genetics:

A:Gene: PrxV

A:Map position: 19

A:Introns: 53/3; 98/2; 141/3; 154/3; 175/2

C:Keywords: liver

Query Match 76.0%; Score 630.5; DB 2; Length 209;

Best Local Similarity 78.0%; Pred. No. 6.1e-51;

Matches 131; Conservative 6; Mismatches 18; Indels 13; Gaps 2;

QY 1 MAPIKVGDALPAVEFEGEPGNKYNLAELFGKKGVLFGVDPGAPFGCSKTHL-----P 54

DB 49 MAPIKVGDALPAVEFEGEPGNKYNLAELFGKKGVLFGVDPGAPFGCSKTHL-----P 101

QY 55 GFVEQAEALKAKGVVACISVNDAPVTGEMGRARHAKGVRLADPTGAFGKETDILLD 114

DB 102 GFVEQAEALKAKGVVACISVNDAPVTGEMGRARHAKGVRLADPTGAFGKETDILLD 161

QY 115 DSIVSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 162

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

DB 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209

QY 162 DSVLSIFGNRRLKRPMSWVODGIVKALNVEEDGGLTCSLAPNIISQL 209



[illegible]

A:Map position: 1	34.5%;	Score 286;	DB 2;	Length 162;
Query Match				

C:Genetics: 1  
A:Gene: F12P19.13  
A:Map position: 1

Query Match	34.5%	Score 286	DB 2	Length 163
Best Local Similarity	40.2%	Pred. No. 3.2e-19		
Matches	68	Conservative	29	Mismatches 58
				Indels 14
				Gaps 6

